



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 110491

TO: Dave Nguyen
Location: CM1/12B15
Art Unit: 1632
Monday, December 22, 2003
Case Serial Number: 09/620607

12E12

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Nguyen,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:39:45 ; Search time 2124 Seconds
(without alignments)
10304.449 Million cell updates/sec

Title: US-09-620-607B-34

Perfect score: 535

Sequence: 1 gcagagacaataatgcgaaga.....aaaaaatgtccctaactgg 535

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sv.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	521.4	97.5	1011	10	BC028879	Mus muscu
2	521.4	97.5	180007	2	AC132933	Mus muscu
3	521.4	97.5	203000	2	AC139212	Mus muscu
4	515.8	96.4	1040	10	AF166097	Mus muscu
5	514.2	96.1	1040	6	BD095993	Immunoaas
6	514.2	96.1	1040	6	BD103482	Immunoaas
7	347.2	64.9	185784	2	AC120860	Mus muscu
8	347.2	64.9	208806	2	AC102491	Mus muscu
9	296.2	55.4	910	10	AF166100	Mus muscu
10	296.2	55.4	332220	2	AC128180	Rattus no
11	146.2	27.3	86186	2	AC133544	Homo sapi
12	146.2	27.3	95202	2	AC140524	Homo sapi
13	146.2	27.3	117774	2	AC140508	Homo sapi
14	146.2	27.3	193633	9	AC009167	Homo sapi
15	146.2	27.3	198276	2	AC145040	Gorilla g
16	144.6	27.0	174634	2	AC140513	Homo sapi
17	144.6	27.0	187359	2	AC140518	Homo sapi
18	144.6	27.0	196341	2	AC140517	Homo sapi
19	144.6	27.0	205443	2	AC140505	Homo sapi
20	144.6	27.0	231174	9	AC139264	Homo sapi
21	144.6	27.0	241278	9	AC097268	Homo sapi
22	131.6	24.6	456	10	AF210429	Mus muscu
23	120	22.4	742	6	AR105919	Sequence
24	120	22.4	742	6	AR211354	Sequence
25	95.2	17.8	1020	6	BD095984	Immunoaas
26	95.2	17.8	1020	6	BD103473	Immunoaas
27	95.2	17.8	1020	9	HS095301	Human calci
28	94	17.6	445	6	AX329696	Sequence
29	94	17.6	445	6	AX335440	Sequence
30	88.4	16.5	159621	9	AC083801	Sequence
31	87.8	16.4	465	6	BD095985	Immunoaas
32	87.8	16.4	465	6	BD103474	Immunoaas
33	86.8	16.2	148116	2	AC078838	Homo sapi
34	78.2	14.6	94673	2	AC009018	Homo sapi
35	42.6	8.0	156959	2	AC136042	Rattus no
36	42.6	8.0	207549	2	AC137021	Rattus no
37	42.6	8.0	212000	2	AC106080	Rattus no
38	42.6	8.0	308087	2	AC128813	Rattus no
39	40	7.5	140120	9	AL390237	Human DNA
40	40	7.5	142126	2	AC026139	Homo sapi
41	40	7.5	178364	2	AC021702	Homo sapi
42	40	7.5	231252	2	AC140137	Homo sapi
43	39.4	7.4	220242	10	AL603706	Mouse DNA
44	38.6	7.2	228000	2	AC135692	Mus muscu
45	38.2	7.1	290029	1	AE017027	Bacillus

ALIGNMENTS

RESULT 1	BC028879	BC028879	1011 bp	mRNA	linear	ROD 16-APR-2003
LOCUS	Mus musculus phospholipase A2, group X, mRNA (cDNA clone MGC:25894					
DEFINITION	IMAGE:4218273), complete cds.					
ACCESSION	BC028879					
VERSION	BC028879.1	GI:22135659				
KEYWORDS	MGC.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
	1 (bases 1 to 1011)					
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,					
	Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,					

Alteschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouford, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalish, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22389257

12477932

2 (bases 1 to 1011)

Strausberg, R.

Direct Submission

Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapsb@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>

Series: IRAK Plate: 31 Row: b Column: 16

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

FEATURES

Location/Qualifiers

1..1011

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="MGC:25894 IMAGE:4218273"

/tissue_type="Colon, normal. 5 month old male mouse."

/clone_lib="NCI CGAP Co24"

/lab_host="DH10B"

/note="vector: pCMV-SPORT6"

1..1011

/genes="p1a2g10"

/note="synonyms: PLA2GX, mCXsPLA2"

/db_xref="LocusID:26565"

/db_xref="MGI:1347522"

33..467

/codon_start=1

/product="p1a2g10 protein"

/protein_id="AAH28879.1"

/db_xref="GI:22135660"

/db_xref="LocusID:26565"

/translation="MLLLLLLLGPGPGFSEATRRSHVYKGLLELAGLTDCVGPERS PMAYMNYGCGLGHGGEPRDAIDWCYHDDCCYSRAQDAGCSFKLDYPPWKCDHDI

gene

CDS

BASE COUNT 263 a 247 c 251 g 250 t

ORIGIN

Query Match

Best Local Similarity 97.5%; Score 521.4; DB 10; Length 1011;

Matches 533; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 1 GCAGAGAAACAATGCCAAGAACTTTTGTGAGGTGTGACGAGGAGCTGGCTTACTGCCTG 60

DB 430 GCAGAGAAACAATGCCAAGAACTTTTGTGAGGTGTGACGAGGAGCTGGCTTACTGCCTG 489

QY 61 GCAGGAGCGAGTACCACCTGAATACCTCTTCTTCCCTCCATTTTATGTGAGAGGAC 120

DB 490 GCAGGAGCGAGTACCACCTGAATACCTCTTCTTCCCTCCATTTTATGTGAGAGGAC 549

QY 121 TCTCCCAAGTCAATTTGACAGGCTCACATGTCCTTTTGCACATGGAAGCGACTTCACTT 180

DB 550 TCTCCCAAGTCAATTTGACAGGCTCACATGTCCTTTTGCACATGGAAGCGACTTCACTT 609

QY 181 TCAGTGATCACCAACAGCATGCAATTTTGTGAGGAGAGTCAACCGAGGCGAAGTCTAAA 240

DB 610 TCAGTGATCACCAACAGCATGCAATTTTGTGAGGAGAGTCAACCGAGGCGAAGTCTAAA 669

QY 241 GCCACTCGGTTGCTTCTTCTTCCATTCAGGAACCTACAACTATGAGCCCTGTGGAGTT 300

DB 670 GCCACTCGGTTGCTTCTTCTTCCATTCAGGAACCTACAACTATGAGCCCTGTGGAGTT 729

QY 301 GCCAGTCTGATGAAGAGTTCAAAGTCTGGGCTGTTTATACAAATTAAGCGCTGTGGTGG 360

DB 730 GCCAGTCTGATGAAGAGTTCAAAGTCTGGGCTGTTTATACAAATTAAGCGCTGTGGTGG 788

QY 361 GCGTGATATCTTTTGAATTCAGCCTTTATGAGAAGCTGTAATCTTGTGACCTGTG 420

DB 789 GCGTGATATCTTTTGAATTCAGCCTTTATGAGAAGCTGTAATCTTGTGACCTGTG 848

QY 421 CAGGCTGCTGTCAGATGTGGTGAAACCTGCTTAGCTTGTGCTGTGTTGTTGTTAATCACTT 480

DB 849 CAGGCTGCTGTCAGATGTGGTGAAACCTGCTTAGCTTGTGCTGTGTTGTTGTTAATCACTT 908

QY 481 GCCACATGATACATCTAAGAATTGTAATTAATAAATAAATAAATAAATAAATAAATAAATAA 535

DB 909 GCCACATGATACATCTAAGAATTGTAATTAATAAATAAATAAATAAATAAATAAATAAATAA 963

AC132933 180007 bp DNA linear HTG 21-FEB-2003

Mus musculus clone RP24-128D9, WORKING DRAFT SEQUENCE, 25 unordered pieces.

AC132933

VERSION AC132933.3 GI:28460829

HTG: HTGS PHASE1; HTGS DRAFT.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 180007)

AUTHORS Birren, B., Nusbaum, C. and Lander, E.

TITLE Mus musculus, clone RP24-128D9

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 180007)

AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgaltier, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hegos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,

O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE JOURNAL

Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE AUTHORS

3 (bases 1 to 180007)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE JOURNAL

Submitted (21-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Feb 21, 2003 this sequence version replaced gi:28269618.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L27253

Center clone name: 128.D.9

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 174258 bases at least Q40

Consensus quality: 175884 bases at least Q30

Consensus quality: 176691 bases at least Q20

Insert size: 177607; sum-of-contigs

Quality coverage: 10.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 33601: contig of 33601 bp in length
* 33602 33701: gap of 100 bp
* 33702 34361: contig of 660 bp in length
* 34362 34461: gap of 100 bp
* 34462 35133: contig of 672 bp in length
* 35134 35233: gap of 100 bp
* 35234 35962: contig of 729 bp in length
* 35963 36062: gap of 100 bp
* 36063 36782: contig of 720 bp in length

* 36783 36882: gap of 100 bp
* 36883 37333: contig of 451 bp in length
* 37333 37433: gap of 100 bp
* 37434 38130: contig of 697 bp in length
* 38131 38230: gap of 100 bp
* 38231 38939: contig of 709 bp in length
* 38940 40065: contig of 1026 bp in length
* 40066 40165: gap of 100 bp
* 40166 40892: contig of 727 bp in length
* 40893 41629: contig of 637 bp in length
* 41630 41729: gap of 100 bp
* 41730 42426: contig of 697 bp in length
* 42427 42526: gap of 100 bp
* 42527 43212: contig of 686 bp in length
* 43213 43312: gap of 100 bp
* 43313 43999: contig of 687 bp in length
* 44000 44099: gap of 100 bp
* 44100 44807: contig of 708 bp in length
* 44808 44907: gap of 100 bp
* 44908 45766: contig of 859 bp in length
* 45767 45866: gap of 100 bp
* 45867 49123: contig of 3257 bp in length
* 49124 49223: gap of 100 bp
* 49224 51352: contig of 2129 bp in length
* 51353 51453: gap of 100 bp
* 51453 59543: contig of 8091 bp in length
* 59544 59644: gap of 100 bp
* 59644 66930: contig of 7287 bp in length
* 66931 78511: contig of 11481 bp in length
* 78512 78611: gap of 100 bp
* 78612 92092: contig of 13481 bp in length
* 92093 92192: gap of 100 bp
* 92193 113443: contig of 21251 bp in length
* 113444 113543: gap of 100 bp
* 113544 153243: contig of 39700 bp in length
* 153244 153343: gap of 100 bp
* 153344 180007: contig of 26664 bp in length.

Location/Qualifiers

1. 180007
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-128D9"
/clone_lib="RPCI-24 Male Mouse BAC"
1. 33601
/note="assembly_fragment"
vector_side:left
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FEATURES source

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

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misc_feature

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misc_feature

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	vector_side:right		

Query Match	97.5%	Score	521.4;	DB 2;	Length	180007;	
Best Local Similarity	99.6%;	Pred. No.	4.8e-156;				
Matches	533;	Conservative	0;	Mismatches	1;	Gaps	1;
QY	1	GCAGAGAACAAATGCCAAGAACTTTTGTGCGAGTGTGACGAGAGCTGGCTTACTGCCTG	60				
DB	173707	GCAGAGAACAAATGCCAAGAACTTTTGTGCGAGTGTGACGAGAGCTGGCTTACTGCCTG	173766				
QY	61	GCAGGACCGAGTACCACTGAAATACCTCTTCTTCCCTCCATTTATGTGAGAGAGC	120				
DB	173767	GCAGGACCGAGTACCACTGAAATACCTCTTCTTCCCTCCATTTATGTGAGAGAGC	173826				
QY	121	TCTCCCAAGTCAATTGACAGGCTCACATGTCCTTTGACATGAAACGCACTTCACTT	180				
DB	173827	TCTCCCAAGTCAATTGACAGGCTCACATGTCCTTTGACATGAAACGCACTTCACTT	173886				
QY	181	TCAGTGATACCAACAGCATGCAATTTGTGAGGAGAGTACCGGAGGCCAAGTGTCTAA	240				
DB	173887	TCAGTGATACCAACAGCATGCAATTTGTGAGGAGAGTACCGGAGGCCAAGTGTCTAA	173946				
QY	241	GCCACCTGCGTTGCTTCTCTCTCCATTCAGGAACCTACAACATATGAGCTGTGGAGTT	300				
DB	173947	GCCACCTGCGTTGCTTCTCTCTCCATTCAGGAACCTACAACATATGAGCTGTGGAGTT	174006				
QY	301	GCCAGTCTGATGAAGGTTCAAGTCTGGCTGTTTATACAATAAGCGCTGTGTGG	360				
DB	174007	GCCAGTCTGATGAAGGTTCAAGTCTGGCTGTTTATACAATAAGCGCTGTGTGG	174065				
QY	361	CGGTGTTATACCTTTTGGAAATTCAGGCTTTATGAGAGCTGTACTATCTTGTACCTGCTG	420				
DB	174066	CGGTGTTATACCTTTTGGAAATTCAGGCTTTATGAGAGCTGTACTATCTTGTACCTGCTG	174125				
QY	421	CAGGCTCTGTCAGATGTGGGTGAACACCTGCTTAGGCTTTGCTGTGGTAAATACAT	480				
DB	174126	CAGGCTCTGTCAGATGTGGGTGAACACCTGCTTAGGCTTTGCTGTGGTAAATACAT	174185				
QY	481	GCCACATGATACATCTAAGAAATGTAACTGTAAATAAAAAATGTTCCCTTAACCTGG	535				
DB	174186	GCCACATGATACATCTAAGAAATGTAACTGTAAATAAAAAATGTTCCCTTAACCTGG	174240				

RESULT 3
AC139212/c
LOCUS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

TITLE	JOURNAL	COMMENT
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Mus musculus chromosome 16 clone RP23-331D17 map 16, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
AC139212
AC139212.3 GI:28628000
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 203000)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 16, clone RP23-331D17
Unpublished
2 (bases 1 to 203000)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Bouckhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Coilymore,A., Cook,A., Cooke,P., Corum,B., DeArckellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
McElrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupa,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (27-JAN-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 203000)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Bouckhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Coilymore,A., Cook,A., Cooke,P., Corum,B., DeArckellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
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Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
McElrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
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Rachupa,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (04-WAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 4, 2003 this sequence version replaced gi:286330048.
All repeats were identified using RepeatMasker:
Snit, A.F.P.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L29145
Center clone name: 331 D 17

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----- Project Information
Center project name: L29145
Center clone name: 331 D 17
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----- Summary Statistics -----
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 201586 bases at least Q40
Consensus quality: 201837 bases at least Q30
Consensus quality: 202010 bases at least Q20
Insert size: 205000; agarose-fp
Insert size: 202300; sum-of-contigs
Quality coverage: 11.6 in Q20 bases; agarose-fp
Quality coverage: 11.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 52046: contig of 52046 bp in length
* 52047 52146: gap of 100 bp
* 52147 53208: contig of 1062 bp in length
* 53209 53308: gap of 100 bp
* 53309 54451: contig of 1143 bp in length
* 54452 54551: gap of 100 bp
* 54552 56935: contig of 2384 bp in length
* 56936 57035: gap of 100 bp
* 57036 59943: contig of 2908 bp in length
* 59944 60043: gap of 100 bp
* 60044 85051: contig of 25008 bp in length
* 85052 85151: gap of 100 bp
* 85152 163137: contig of 77986 bp in length
* 163138 163237: gap of 100 bp
* 163238 203000: contig of 39763 bp in length.

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Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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LOCUS Mus musculus group X secreted phospholipase A2 (Pla2g10) mRNA,
DEFINITION complete cds.
ACCESSION AF166097
VERSION AF166097.2 GI:5525307
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1040)
AUTHORS Valentini, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G.
TITLE On the diversity of secreted phospholipases A(2). Cloning, tissue
distribution, and functional expression of two novel mouse group II
enzymes
J. Biol. Chem. 274 (44), 31195-31202 (1999)
JOURNAL MEDLINE 20002639
PUBMED 10531313
REFERENCE 2 (bases 1 to 1040)
AUTHORS Valentini, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1999) IPMC, CNRS, 660, route des Lucioles,
Valbonne 06560, France
REFERENCE 3 (bases 1 to 1040)
AUTHORS Valentini, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-1999) IPMC, CNRS, 660, route des Lucioles,
Valbonne 06560, France
REMARK Sequence update by submitter
COMMENT On Dec 6, 1999 this sequence version replaced gi:6164695.
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BASE COUNT 244 a 258 c 277 g 261 t
ORIGIN

Query Match      96.4%; Score 515.8; DB 10; Length 1040;
Best Local Similarity 99.4%; Pred. No. 1.4e-154; Indels 1; Gaps 1;
Matches 528; Conservative 0; Mismatches 2;

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DB 493 GCAGAGAACAAATGCCAAGAACTTTTGTGACAGGTGTGACGAGAGCTGGCTTACTGCCTG 552
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DB 553 GCAGGACCGAGTACACCTGAAATACCTCTTCTCCCTCCATTTATATGTGAGAGGAC 612
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DB 733 GCACCTGCTGTTGCTTCTTCCATTCAGGAACCTCAACATATGAGGCTGTGGAGTT 792
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DEFINITION Immunoassay for group X phospholipase A2.
ACCESSION BD095993
VERSION    BD095993.1 GI:22641581
KEYWORDS   WO 0190195-A/10.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            (bases 1 to 1040)
REFERENCE  1
AUTHORS   Hanasaki, K., Imagawa, K. and Masuta, K.
TITLE     Immunoassay for group X phospholipase A2
JOURNAL   Patent: WO 0190195-A/10 29-NOV-2001.
            SHIONOGI & CO LTD, KOJI HANASAKI, KEIICHI IMAGAWA, KEIICHI MASUTA

COMMENT OS Mus musculus (mouse)
PN WO 0190195-A/10
PD 29-NOV-2001
PF 21-NOV-2000 WO 2000JP008198
PR 24-MAY-2000 JP OOP 152967
PI KOJI HANASAKI, KEIICHI IMAGAWA, KEIICHI MASUTA
PC C07K16/40, A61K39/395, A61P43/00, G01N33/53, G01N33/573, G01N33/574
CC Immunoassay for group X phospholipase A2
FH Key Location/Qualifiers
FT CDS (175)..(630).

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Best Local Similarity 99.2%; Pred. No. 4.5e-154; Indels 1; Gaps 1;
Matches 527; Conservative 0; Mismatches 3;

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DEFINITION Immunoassay for group X phospholipase A2.
ACCESSION BD103482
VERSION    BD103482.1 GI:22649056
KEYWORDS   WO 0190196-A/10.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            (bases 1 to 1040)
REFERENCE  1
AUTHORS   Hanasaki, K., Imagawa, K. and Masuta, K.
TITLE     Immunoassay for group X phospholipase A2

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JOURNAL	Patent: WO 0190196-A 10 23-NOV-2001;
COMMENT	SHIONOGI & CO LTD, KOJI HANASAKI, KEIICHI IMAGAWA, KEIICHI MASUTA
OS	Mus musculus (mouse)
PN	WO 0190196-A/10
PD	29-NOV-2001
PP	22-MAY-2001 WO 2001JP004267
PR	24-MAY-2000 JP OPF 152967, 21-NOV-2000 WO PCTJP0008198 PI
KOJI HANASAKI, KEIICHI IMAGAWA, KEIICHI MASUTA	
PC	CO7K16/40, C12N9/16, C12P21/08, A61K39/395, G01N33/53, G01N33/574,
PC	G01N33/576
CC	Immunosay for group X phospholipase A2
PH	Key
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BASE COUNT	243 a 258 c 278 g 261 t
ORIGIN	
Query Match	96.1%; Score 514.2; DB 6; Length 1040;
Best Local Similarity	99.2%; Pred. No. 4.5e-154;
Matches 527; Conservative 0; Mismatches 3; Indels 1; Gaps 1;	
Qy	1 GCAGAGAACAAATGCCAAGACTTTTGTGAGGTGTGACAGAGCTGGCTTACTGCTG 60
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493	GCAGAGAACAGATGCCAAGACTTTTGTGAGGTGTGACAGAGCTGGCTTACTGCTG 552
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DEFINITION	Mus musculus clone RP23-26110, WORKING DRAFT SEQUENCE, 7 unordered pieces.
ACCESSION	AC120860
VERSION	AC120860.3 GI:28876105
KEYWORDS	HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 185784)

Birren,B., Nusbaum,C. and Lander,E.

Mus musculus, clone RP23-26110

Unpublished

2 (bases 1 to 185784)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (13-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 185784)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArelano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (07-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 7, 2003 this sequence version replaced gi:28195444.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L22304

Center code: 26110

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 183652 bases at least Q40

Consensus quality: 184566 bases at least Q30

Consensus quality: 184947 bases at least Q20

Insert size: 183000; agarose-fp

Insert size: 185184; sum-of-contigs

Quality coverage: 9.9 in Q20 bases; agarose-fp

Quality coverage: 9.8 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1979: contig of 1979 bp in length
 * 1980: gap of 100 bp
 * 2080: contig of 10560 bp in length
 * 12640: gap of 100 bp
 * 12740: contig of 16132 bp in length
 * 28872: gap of 100 bp
 * 28972: contig of 16882 bp in length
 * 45854: gap of 100 bp
 * 45954: contig of 97836 bp in length
 * 143790: gap of 100 bp
 * 143890: contig of 20662 bp in length
 * 164552: gap of 100 bp
 * 164652: contig of 21133 bp in length.

FEATURES

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Query Match 64.9%; Score 347.2; DB 2; Length 185784;

Best Local Similarity 87.2%; Pred. No. 6.8e-100;

Matches 441; Conservative 0; Mismatches 53; Indels 12; Gaps 5;

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 Db 177587 TGTGTGCGAGTGTGACGAGGCTGGCTTACTGCTGGCAGGACCGAGTACCACCTGGAG 177646
 QY 84 ATACTCTTCTTCCCTCCATTTTATGTGAGAGGACTCTCCCAAGTGCAATTGACAGGC 143
 Db 177647 ATACTCTTCTTCCCTCCATTTTATGTGAGAGGACTCTCCCAAGTGCGAGTACCACAGGC 177706
 QY 144 TCACATGTCCTTTGGCAGTGAACGACATTCATCTTTAGTGTATCCACACGACATGCA 203
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 Db 177937 AACCTTTATGAACGCTGTACTATCTTCTACTCTGTTCAGAGGGTGTGGTGCAGATGTG 177996
 QY 442 GGTGAACACCTGCTTAGGCTTTGCTGTGTGTAATAACATTCGCCACATGATACATCTAAGAA 501
 Db 177997 GATGAACACCTGCTTAGGCTTGGCTGTAGTATAACATTCGCCACATGATACATCTAAGAA 178056
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 Db 178057 TTGTAACTGTATAAATAAATGTTCC 178082

RESULT 8
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 Mus musculus clone RP24-529L13, WORKING DRAFT SEQUENCE, 36
 unordered pieces.
 AC102491
 AC102491.2 GI:22380884
 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 Mus musculus (house mouse)
 Mus musculus
 Mus musculus
 Birren,B., Nusbaum,C. and Lander,B.
 1 (bases 1 to 208806)
 Mus musculus, clone RP24-529L13
 2 (bases 1 to 208806)
 Unpublished
 Birren,B., Linton,L., Nusbaum,C., Lander,B., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Kamat,A., Karatag,A., Kells,C., LaRocque,K.,
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J.,
 Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 208806)
 Birren,B., Nusbaum,C., Lander,B., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
 Cooke,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,

TITLE
JOURNAL

COMMENT

Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J.T., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Minova,T., Milenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuppach,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zemlek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Aug 21, 2002 this sequence version replaced gi:17061577.

All repeats were identified using RepeatMasker:

Smit, A.F.A., Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Web code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L18907

Center clone name: 529_L13

----- Summary Statistics

* Sequencing vector: Plasmid; n/a; 100% of reads

* Assembly program: Phrap; version 0.960731

* Consensus quality: 196684 bases at least Q40

* Consensus quality: 202269 bases at least Q30

* Consensus quality: 204312 bases at least Q20

* Insert size: 211000; agarose-fp

* Insert coverage: 205306; sum-of-contigs

* Quality coverage: 6.3 in Q20 bases; agarose-fp

* Quality coverage: 6.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 665: contig of 665 bp in length

* 666 785: gap of 100 bp

* 766 1527: contig of 762 bp in length

* 1528 1627: gap of 100 bp

* 1628 2254: contig of 627 bp in length

* 2255 2354: gap of 100 bp

* 2355 2981: contig of 627 bp in length

* 2982 3081: gap of 100 bp

* 3082 3780: contig of 699 bp in length

* 3781 3880: gap of 100 bp

* 3881 4930: contig of 1050 bp in length

* 4931 5030: gap of 100 bp

* 5031 5688: contig of 638 bp in length

* 5689 5769: gap of 100 bp

* 5769 6562: contig of 794 bp in length

* 6563 6662: gap of 100 bp

* 6663 7624: contig of 962 bp in length

* 7625 7724: gap of 100 bp

* 7725 8843: contig of 1119 bp in length

* 8844 9679: gap of 100 bp

* 9679 9779: contig of 736 bp in length

* 9680 9779: gap of 100 bp

* 9780 10568: contig of 789 bp in length

* 10569 10688: gap of 100 bp

* 10689 11530: contig of 862 bp in length

* 11531 11630: gap of 100 bp

* 11631 12340: contig of 710 bp in length

* 12340 12340: contig of 710 bp in length

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Best Local Similarity 87.2%; Pred. No. 6.9e-100;
Matches 441; Conservative 0; Mismatches 53; Indels 12; Gaps 5;

QY 24 TTGTGTCAGTGTGACGAGAGTGGCTTACTGCTGGCAGGACCGAGTACCACCTGAA 83
DB 186234 TGTGTGAGGTGTGACGAGAGTGGCTTACTGCTGGCAGGACCGAGTACCACCTGAG 186293
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QY 384 AGCTTTATGAGAGTGTACTATCTTGTACCTCTGCG--AGGCTGCTGTGATGATG 441
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RESULT 9
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LOCUS Rattus norvegicus group X secreted phospholipase A2 mRNA, complete cds.
DEFINITION
ACCESSION AF166100
VERSION AF166100.1 GI:6164701
KEYWORDS Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 910)
AUTHORS Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
TITLE On the diversity of secreted phospholipases A(2). Cloning, tissue distribution, and functional expression of two novel mouse group II enzymes
J. Biol. Chem. 274 (44), 31195-31202 (1999)
MEDLINE 20002639
PUBMED 10531313
REFERENCE 2 (bases 1 to 910)
AUTHORS Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1999) IPWC, CNRS, 660, route des Lucioles,

FEATURES
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BASE COUNT 224 a 216 c 235 g 235 t
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Best Local Similarity 80.3%; Pred. No. 8.2e-84;
Matches 425; Conservative 0; Mismatches 88; Indels 16; Gaps 6;

QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGCTGGCTTACTGCTG 60
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QY 421 C--AGGCTGCTGTGATGAGTGGTGAACACCTGCTTGGCTTGGCTTGGTGAATAACA 478
DB 781 CAGAGGGTGTGGTGGTCAAA-----TGAACACCTGCTTGGCTTGGCTTGGTGAATAACA 834
QY 479 TTGCCCATGATACATCATTAAGATTCGTAATCTGAATAAAAAAATGTTCC 527
DB 835 TTGCCAC--GATACATCTAGGAATTTGTAGTGAATAAAGCAATGTTCCC 881

RESULT 10
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DEFINITION Rattus norvegicus clone CH230-373N16, *** SEQUENCING IN PROGRESS
***, 11 unordered pieces.
ACCESSION AC128180
VERSION AC128180.2 GI:23908197
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 33220)
AUTHORS Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
TITLE On the diversity of secreted phospholipases A(2). Cloning, tissue distribution, and functional expression of two novel mouse group II enzymes
J. Biol. Chem. 274 (44), 31195-31202 (1999)
MEDLINE 20002639
PUBMED 10531313
REFERENCE 2 (bases 1 to 910)
AUTHORS Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1999) IPWC, CNRS, 660, route des Lucioles,
```

AUTHORS

Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angilano, D., Ayalebechi, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biewalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, J., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hayes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howell, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuewa, L., Loulsged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankwelen, O., Okwunonu, G., Olarnpunseagoon, A., Pal, S., Parks, K., Pastorek, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinfeld, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, P., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

TITLE
JOURNAL

REFERENCE
2 (bases 1 to 332220)
Unpublished

AUTHORS

Worley, K.C.

TITLE
JOURNAL

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS

3 (bases 1 to 332220)

TITLE
JOURNAL

Rat Genome Sequencing Consortium.

TITLE
JOURNAL

Submitted (12-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GZNT
Center clone name: CH230-373N16
Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 210811 bases at least Q40
Consensus quality: 214286 bases at least Q30
Consensus quality: 216531 bases at least Q20
Estimated insert size: 223402; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 60608: contig of 60608 bp in length
* 60609 60708: gap of unknown length
* 60709 65888: contig of 5180 bp in length
* 65889 65988: gap of unknown length
* 65989 98233: contig of 32245 bp in length
* 98234 98333: gap of unknown length
* 98334 103602: contig of 5269 bp in length
* 103603 103702: gap of unknown length
* 103703 123008: contig of 19306 bp in length
* 123009 123108: gap of unknown length
* 123109 308919: contig of 185711 bp in length
* 308920 308919: gap of unknown length
* 308920 320683: contig of 11764 bp in length
* 320684 320783: gap of unknown length
* 320784 322464: contig of 1681 bp in length
* 322465 322565: gap of unknown length
* 322565 324599: contig of 2034 bp in length
* 324599 326126: gap of unknown length
* 326127 326226: contig of 1428 bp in length
* 326227 332220: contig of 5994 bp in length.

FEATURES

source

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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-373N16"
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/note="wgs end extension
clone end:Sp6"

misc_feature

3530..4800
/note="wgs end extension
clone end:Sp6"

misc_feature

10041..10946
/note="clone boundary
clone end:Sp6
site:Mbol
end_sequence:RXAWB80TV"

misc_feature

98334..99677
/note="wgs contig"

misc_feature

103703..104958
/note="wgs contig"

misc_feature

116648..117691
/note="wgs contig"

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/notes="wgs contig"
misc_feature 125742..128797
/notes="wgs contig"
misc_feature complement(182596..183504)
/notes="clone_boundary
clone end:T7"
site:Mbol
end sequence:RXW80TJ"
misc_feature 306849..308819
/notes="wgs end_extension
clone end:T7"
misc_feature 308920..310257
/notes="wgs end_extension
clone end:T7"
misc_feature 310784..315075
/notes="wgs end_extension
clone end:T7"
misc_feature 316152..320683
/notes="wgs end_extension
clone end:T7"
BASE COUNT 64872 a 48021 c 47726 g 57171 t 114430 others
ORIGIN
Query Match 55.4%; Score 296.2; DB 2; Length 332220;
Best Local Similarity 79.1%; Pred. No. 2.1e-83;
Matches 417; Conservative 0; Mismatches 98; Indels 12; Gaps 5;
Qy 1 GCAGAGAACAAATCCAGAGACTTTCTGCAGGTGTCAGGAGCTGGCTTACTGCTG 60
Db 282163 GCAGAGAACAAATCCAGAGACTCTATGCAAGGTGTGATGAGCGCTGCATCTGCTG 282222
Qy 61 GCAGGGACCGAGTACCACTGAATACCTCTCTCCCTCCCTCAATTTATGTGAGAGGAC 120
Db 282223 GCAGACAGATGATACCACTGAATACCTCTCTCCCTCGGTATTTATGTGAGAGGAC 282282
Qy 121 TCTCCCAAGTGCAATGACAGGCTCAATGTCCTTTGCGATGCAATGGAACGCACTTCACTT 180
Db 282283 TCACCCAAAGTGCAACTAATAGGCTGAAATGTCCCTTTGCGATGCAATGGAATGCAATGCTT 282342
Qy 181 TCAGTGATACCAACAGCATGCAATTTGTGCGAGAGTACCGAGGCGCAAGTGCTAAA 240
Db 282343 TCAGTGATGAAACACAGCTTCGATTTGCGGAG--GAGTCCCTGAGGCCAAGTGATGAA 282400
Qy 241 GCCACCTGCGTTTGTCTTTCTCTCCATTCAGGAACTCACAACTATGAGCTGTGGAGTT 300
Db 282401 G---CCTGGGTTTGTCTTTCTCCCTCCATTCGTGAACCTCAGGACTATGAGCTGTGGAGCT 282457
Qy 301 GCCAGTCTGATGAAGGTTCAAAGTCTGGGCTGTTTATACAAATGAAGCGCTGTGTGG 360
Db 282458 GCCAGTTTGTATGAAGGTTGAGAGTCTGGGCTGTTTATACAACT-GCAACTGTGTGG 282516
Qy 361 GCGTGTATACCTTTTGAAATTCAGCTTTATGAGAGCTGTACTATCTGTACTGCTG 420
Db 282517 GCITGATATAATTTTGAAGTCCAACTTTACAAAAGCTTTACTACTGTGTAACTGCTG 282576
Qy 421 CAGGCTGCTGCTGATGATGGTGGAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 480
Db 282577 CAGAG---GTTGTGTGTCAAATGAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 282632
Qy 481 GCCACATGATACATCTAAGATTGTAAGTGAATGAATGAATGAATGAATGAATGAATGAAT 527
Db 282633 GCCAC--GATACATCTAGGAATTTGTAAGTGAATGAATGAATGAATGAATGAATGAAT 282677
RESULT 11
AC133544/c 86186 bp DNA linear HTG 14-SEP-2002
LOCUS Homo sapiens chromosome 16 clone RP11-115C1, WORKING DRAFT
DEFINITION SEQUENCE, 5 unordered pieces.
ACCESSION AC133544
VERSION AC133544.1 GI:22857540
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 86186)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 86186)
DOE Joint Genome Institute.
Direct Submission
Submitted (14-SEP-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 450574
Center clone name: RPCI-11_115C1

Summary Statistics
Consensus quality: 84676 bases at least Q40
Consensus quality: 85119 bases at least Q30
Consensus quality: 85392 bases at least Q20
Estimated insert size: 110000; agarose-fp estimation
Estimated insert size: 85786; sum-of-contigs estimation
Quality coverage: 14.87 in Q20 bases; agarose-fp estimation
Quality coverage: 19.07 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1138: contig of 1138 bp in length
* 1139 1238: gap of unknown length
* 1239 7458: contig of 6220 bp in length
* 7459 7558: gap of unknown length
* 7559 23435: contig of 15877 bp in length
* 23436 23535: gap of unknown length
* 23536 36643: contig of 13108 bp in length
* 36644 36743: gap of unknown length
* 36744 86186: contig of 49443 bp in length.
Location/Qualifiers
1..86186
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-115C1"
/clone_lib="RPCI human BAC library 11"
BASE COUNT 23562 a 20274 c 20394 g 21556 t 400 others
ORIGIN
Query Match 27.3%; Score 146.2; DB 2; Length 86186;
Best Local Similarity 66.0%; Pred. No. 3.7e-35;
Matches 315; Conservative 0; Mismatches 133; Indels 29; Gaps 6;
Qy 1 GCAGAGAACAAATCCAGAGACTTTTGTGAGGTGTGACGAGAGCTGGCTTACTGCTG 60
Db 48365 GCAGAGAACAAATCCAGAGACTGTTGTGCAAGTGTGACGAGAGATTGCTAAGCTT 48306
Qy 61 GCAGGGACCGAGTACCACTGAATACCTCTCTCCCTCCCTCAATTTATGTGAGAGGAC 120
Db 48305 GCCAAACTGAGTACAACTTAAAGTACCTCTCTTACCCCGAGTTCCTTATGTAGCCGAC 48246
Qy 121 TCTCCCAAGTGCAATTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 174
Db 48245 TCGCCCAAGTGTGACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 48186

QY 175 TCACCTTCAGTATCACCACAGCATGCAATTTGTGCAGAGAGTCAACCGAGGCCAAGT 234
 Db 48185 GTCCCTCTCAGTATGAAACACAGCATTCAGTTATTTGCGAGA-AGGGAACCGAAGCCAAGT 48127
 QY 235 GCTAAAGCCA---CCTGGGTTGCTTCTCCCTCCATTCCAGCACTCAACAATGAGC 290
 Db 48126 GATTAAGCCACACCTTGTTGCTTCTCCCTCCATCCAGCACTCAGGACTGGAGCC 48067
 QY 291 CTGTGAGTGTCCAGTCTGATGAAGGTTCAAAGTCTCTGGGCTCTGTTTATACAAATA--- 347
 Db 48066 CATGTGGTTG-----CAGTTAAAGGCCAAAGCTCTGCGACCTATTTTATAAACTATGA 48012
 QY 348 -----AGCGTGTGTTGGGCGTGTATACCTTTTGAATTCACGCTTTATGAGAAGC 399
 Db 48011 CTGTGTTTATCACTGTGTGGGTCGGTTCCTCATTTTGAGGTTCCATCTTTATGAAAGA 47952
 QY 400 TGTACTATCTTGA---CCTGCTCAGGCTGCTGGTCAAGTGGGTGAACACCTGC 454
 Db 47951 TAACCTGCTTCTTAACCTGCTGGATGGCTGTGATGATCAATGTAAGCAACACCTAC 47895

RESULT 12
 AC140524
 LOCUS
 DEFINITION Homo sapiens chromosome 16 clone RP11-92J23, WORKING DRAFT
 AC140524
 ACCESSION
 VERSION AC140524.1 GI:28557858
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 16
 JOURNAL Unpublished
 REFERENCE
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (25-FEB-2003) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT
 -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>

 Project Information
 Center Project Name: 441932
 Center clone name: RPCI-11_92J23

 Summary Statistics
 Consensus quality: 93140 bases at least Q40
 Consensus quality: 93413 bases at least Q30
 Consensus quality: 93605 bases at least Q20
 Estimated insert size: 175000; agarose-fp estimation
 Estimated insert size: 94702; sum-of-ctigs estimation
 Quality coverage: 12.74 in Q20 bases; agarose-fp estimation
 Quality coverage: 23.54 in Q20 bases; sum-of-ctigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1338: contig of 1338 bp in length
 * 1339 1438: gap of unknown length
 * 1439 4421: contig of 2983 bp in length
 * 4422 4521: gap of unknown length
 * 4522 13613: contig of 9092 bp in length

* 13614 13713: gap of unknown length
 * 13714 33890: contig of 20177 bp in length
 * 33891 33990: gap of unknown length
 * 33991 62933: contig of 28943 bp in length
 * 62934 63033: gap of unknown length
 * 63034 95202: contig of 32169 bp in length.
 FEATURES
 Location/Qualifiers
 1..95202
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-92J23"
 /clone_lib="RPCI human BAC library 11"
 BASE COUNT 24147 a 22297 c 22026 g 26232 t 500 others
 ORIGIN
 Query Match 27.3%; Score 146.2; DB 2; Length 95202;
 Best Local Similarity 66.0%; Pred. No. 3.8e-35; Indels 29; Gaps 6;
 Matches 315; Conservative 0; Mismatches 133;
 QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGAGCTGGCTTACTGSCCTG 60
 Db 50203 GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGAGATTCTTAACCTGCTTA 50262
 QY 61 GCAGGACCGAGTACCACTGAAATACCTCTTCTCCCTCCATTTTATGTGAGAAGGAC 120
 Db 50263 GCCCAACTGAGTACAACTTAAAGTACCTCTTCTACCCCCAGTTCTTATGTGAGCGGAC 50322
 QY 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGCTCCCTTGCACATGGAACGCACT 174
 Db 50323 TGCCCAAGTGTGACTGACTTACTTGCATTGGAATGCTCTTTTGACAGGAATAAAGC 50382
 QY 175 TCACCTTCAGTGAATCAACCAAGCATGCAATTTGTGAGGAGAGTCAACCGAGGCCAAGT 234
 Db 50383 GTCCTCTCAGTAAATGAACAACAGCATTCAGTTATTGTCAGA-AGGGAACCGAAGCCAAGT 50441
 QY 235 GCTAAAGCCA-----CCTGGTGTGCTTCTCTCCATTCCAGCACTCAACAATGAGC 290
 Db 50442 GATAAAGCCCAACACCTTGTGTTGCTTCTCCCTCCCAATCCAGCACTCAGGACTGGAGCC 50501
 QY 291 CTGTGAGTGTCCAGTCTGATGAAGGTTCAAAAGTCTCGGCTGTTTATACAAATA--- 347
 Db 50502 CATGTGGTTG-----CAGTTAAAGCCAAAGTCTCGCACCTATTTTATAAACTATGA 50556
 QY 348 -----AGCGCTGTGTTGGCGTGTATACCTTTTGAATTCAGCCTTTATGAGAAGC 399
 Db 50557 CTGTGTTTATCACTGTGTTGGGTCGGTTCCTTTTGAGGTTCCATCTTTATGAAAAGA 50616
 QY 400 TGTACTATCTTGA---CCTGCTGAGGGCTGCTGGTCAAGTGGGTGAACACCTGC 454
 Db 50617 TAACCTGCTTCTTAACCTGCTTGGATGGTGTAGTCAAATGTGAACGACACCTAC 50673
 RESULT 13
 AC140508
 LOCUS
 DEFINITION Homo sapiens chromosome 16 clone RP11-121D10, WORKING DRAFT
 AC140508
 ACCESSION
 VERSION AC140508.1 GI:28557842
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 16
 JOURNAL Unpublished
 REFERENCE
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission

JOURNAL Submitted (25-FEB-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 452911
Center clone name: RPCI-11_121D10

Summary Statistics
Consensus quality: 114212 bases at least Q40
Consensus quality: 114858 bases at least Q30
Consensus quality: 115531 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 116974; sum-of-contigs estimation
Quality coverage: 13.07 in Q20 bases; agarose-fp estimation
Quality coverage: 19.56 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1159: contig of 1159 bp in length
* 1160 1259: gap of unknown length
* 1260 2760: contig of 1501 bp in length
* 2761 2860: gap of unknown length
* 2861 7171: contig of 4311 bp in length
* 7172 7272: gap of unknown length
* 7272 11692: contig of 4421 bp in length
* 11693 11792: gap of unknown length
* 11793 18058: contig of 6266 bp in length
* 18059 18158: gap of unknown length
* 18159 24831: contig of 6673 bp in length
* 24832 24931: gap of unknown length
* 24932 53782: contig of 28851 bp in length
* 53783 53882: gap of unknown length
* 53883 93841: contig of 39959 bp in length
* 93842 93942: gap of unknown length
* 93942 117774: contig of 23833 bp in length.

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-121D10"
/clone.lib="RPCI human BAC library 11"
BASE COUNT 30315 a 27527 c 27197 g 31935 t 800 others

ORIGIN
Query Match 27.3%; Score 146.2; DB 2; Length 117774;
Best Local Similarity 66.0%; Pred. No. 3.9e-35;
Matches 315; Conservative 0; Mismatches 133; Indels 29; Gaps 6;
QY 1 GCAGAGAACAAATCCCAAGACTTTTGTGAGGTGACGAGGAGCTGCTTACTGCTG 60
DB 41202 GCAGAGAACAAATCCCAAGACTTTGTCAGGTGTCACGAGGAGTGTCTTAACTGCTTA 41261
QY 61 GCAGGACCGAGTACCACTGAATACCTCTTCTCCCTCCATTTATGTGAGAGGAC 120
DB 41262 GCCCAACTGAGTACAACTTAAGTACTCTTCTACCCCGAGTTCCTATGTGACCGGAC 41321
QY 121 TCTCCCAAGTCAATGACAGGC-----TCACATGTCCTTTGCACATGGAACGGCACT 174
DB 41322 TCGCCCAAGTGTGACTGACTACTACCTTGACTTGAATGCTCTTTGCACAAAGGAATAAGC 41381
QY 175 TCACCTTCAGTGTATCCACACAGCATGCAATTTGTGAGGAGATCCACGAGCCCAAGT 234

Db 41382 GTCTCTCTAGTATGAACACAGCAATTCAGTTATTTTGCAGA-AGGAAACCGAAGCCAGT 41440
QY 235 GCTAAAGCCA-----CCTGCGTTTGTCTTCTCCTTCATTCAGGAACCTCAACTATGAGC 290
DB 41441 GATAAAGCCACAACTTGTGTTTGTCTTCCCTCCCAATCCAGAACTCAGGACTGGAGCC 41500
QY 291 CTGTGGAGTTGCCAGTCTGATCAAGGTTCAAAAGTCTGGGCTGTTTATACAAATA-- 347
DB 41501 CATGTGTTTG-----CAGTTAAAGGCCAAAGTCTCGACCTATTTTATAAACTATGA 41555
QY 348 -----AGCGCTGTGTTGGCGGTGATATCTTTTGAATTCAGCCTTTATGAGAAGC 399
DB 41556 CTGTGTTTATCACTGTGTTGGGTCGTTCCATTTTGGAGTTCCATCTTTATGAAAGA 41615
QY 400 TGTACTATCTTCTA--CCTGCTGCAGGGCTGCTGTCAGATGTGGGTGAACACCTGCG 454
DB 41616 TAACTGCTCTCTTAACCTGCTTGGATGCTGCTAGTCAATGTGAACGAACACCTAC 41672

RESULT 14
AC009167 193633 bp DNA linear PRI 18-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-82018, complete sequence.
DEFINITION AC009167
ACCESSION AC009167
VERSION AC009167.9 GI:29029222
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 193633)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 193633)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 193633)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 193633)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 18, 2003 this sequence version replaced gi:17298590.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.

FEATURES
source
1. 193633
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-82018"
BASE COUNT 50384 a 42572 c 43743 g 56934 t

ORIGIN
Query Match 27.3%; Score 146.2; DB 9; Length 193633;
Best Local Similarity 66.0%; Pred. No. 4.2e-35;
Matches 315; Conservative 0; Mismatches 133; Indels 29; Gaps 6;

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QY 1 GCAGAGCAAAATCCCAAGAACTTTGTGAGGTGTGACGAGGAGTGGCTTACTGCTG 60
Db 49087 GCAGAGCAAAATCCCAAGAACTTTGTGAGGTGTGACGAGGAGTGGCTTACTGCTTA 49146
QY 61 GCAGGAGCCAGTACCACTGAAATACCTTCTTCCCTCCCTCCATTTTATGTGAGAGGAC 120
Db 49147 GCCCAAACTGAGTACAACTTAAAGTACCTCTTCTTACCCCGAGTTCCTATGTGAGCCGGAC 49206
QY 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGTCCCTTTGTCACATGGAACGCACT 174
Db 49207 TCGCCCAAGTGTGACTGACTACCTTGTGAAATGCTCTTTGCAAGGAATAAAGC 49266
QY 175 TCACCTTCAGTATCACAACAGATGCAATTTGTGAGAGAGTACACGGAGGCCAAGT 234
Db 49267 GTCTCTCTCAGTAATGAACAACAGCAATTCAGTATTTTGCAGA-AGGGAACCGAAGCAAGT 49325
QY 235 GCTAAAGCCCA---CCTGCGTTTGTCTTCTTCTTCCATTCAGGAACCTCACAACTATGAGC 290
Db 49326 GATTAAGCCCAACCTTGTCTTCTTCTTCCATTCAGGAACCTCACAACTATGAGC 49385
QY 291 CTGTGGAGTTGCCAGTCTGATGAAGTTCAAAGTCTGGGCTGTCTTTTATACAAATA--- 347
Db 49386 CATGTGTTTG-----CAGTTAAAGGCCAAAGTCTGACCTATTTTATAAACTATGA 49440
QY 348 -----ACGCTGTGTGGCGTGATACATCTTTTGAATTCAGCCTTTATGAGAGC 399
Db 49441 CTGTGTTTATCACTGTGTGGGTCGGTTCATTTTGGAGTTCCTCATCTTTATGAAAGA 49500
QY 400 TGTACTATCTTGTGA---CCTGCTGAGGCTGCTGTCAGATGGGTGAACACCTGC 454
Db 49501 TAACCTGTCTTCTAACTGTGATGGCTGTAGTCAAAATGGAACGAACACTAC 49557

RESULT 15
AC145040
LOCUS
DEFINITION
  Gorilla gorilla gorilla clone CH255-165B15, WORKING DRAFT SEQUENCE,
  14 unordered pieces.
ACCESSION
  AC145040.1 GI:31376426
VERSION
  HTG: HTGS PHASE1; HTGS DRAFT.
KEYWORDS
  Gorilla gorilla gorilla (lowland gorilla)
SOURCE
  Gorilla gorilla gorilla
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
REFERENCE
  1 (bases 1 to 198276)
  Eichler, B.E., Johnson, M.E., Antonellis, A., Avele, K.,
  Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
  Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Chu, G.,
  Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Gupta, J.,
  Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurler, B.,
  Idol, J.R., Karlins, E., Kwong, P., Latic, P., Lee-Lin, S.-Q.,
  Lesaghi, R., Maduro, Q.L., Maduro, V.B., Margulies, B.H., Mastello, C.,
  Maskeri, B., McDowell, J., Pagnirigan, C., Pearson, R., Portnov, M.E.,
  Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K.,
  Sison, C., Stantrop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V.,
  Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
  NISC Comparative Sequencing Initiative
  Unpublished
  2 (bases 1 to 198276)
  Green, E.D.

JOURNAL
REFERENCE
  Direct Submission
AUTHORS
  Submitted (04-JUN-2003) NIH Intramural Sequencing Center, 8717
  Grove Avenue Circle, Gaithersburg, MD 20877, USA
JOURNAL
COMMENT
  ----- Genome Center
  Center: NIH Intramural Sequencing Center
  Center code: NISC
  Web site: http://www.nisc.nih.gov
  Contact: nisc.zoo@nih.gov
  ----- Project Information
  Center project name: enl
  Center clone name: 165B15
  ----- Summary Statistics
```

```
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 194149 bases at least Q40
Consensus quality: 195069 bases at least Q30
Consensus quality: 195474 bases at least Q20
Insert size: 155000; agarose-fp
Quality coverage: 11.60x in Q20 bases; agarose-fp
Quality coverage: 9.13x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1 2329: contig of 2329 bp in length
* 2330 2429: gap of unknown length
* 2430 7667: contig of 5238 bp in length
* 7668 7768: gap of unknown length
* 7769 10462: contig of 2695 bp in length
* 10463 10563: gap of unknown length
* 10564 17003: contig of 6341 bp in length
* 17004 23921: contig of 6918 bp in length
* 23922 28476: gap of unknown length
* 28477 28575: gap of unknown length
* 28576 39853: contig of 11177 bp in length
* 39854 50371: gap of unknown length
* 50372 50471: contig of 10518 bp in length
* 50472 69021: contig of 18550 bp in length
* 69022 86311: contig of 17190 bp in length
* 86312 114284: contig of unknown length
* 114285 114383: gap of unknown length
* 114384 137377: contig of 22993 bp in length
* 137378 137476: gap of unknown length
* 137477 161997: contig of 24520 bp in length
* 161998 198276: gap of unknown length
* 198277 198276: contig of 36180 bp in length.
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  /clone_id="CH255"
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  1..2329
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  clone_end:T7
  vector_side:left
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  2430..7667
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86411..114283
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114384..137376
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137477..161996
misc_feature /note="assembly_fragment"
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vector side:left
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54298 a 47009 c 45078 g 50585 t 1306 others
ORIGIN

Query Match 27.3% Score 146.2; DB 2; Length 198276;
Best Local Similarity 66.0%; Pred. No. 4.3e-35;
Matches 315; Conservative 0; Mismatches 133; Indels 29; Gaps 6;

Qy 1 GCAGAGAACAAATGCCCAAGAACTTTGTGCAAGTGTGACGAGGAGCTGGCTTACTGCCTG 60
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Qy 73773 GCAGAGAACAAATGCCCAAGAACTTTGTGCAAGTGTGACGAGGAGCTGGCTTACTGCCTG 73832
Db |||||||
Qy 61 GCAGGAGCCGAGTACCACTGAATACTCTCTTCCCTCCCAATTTTATGTGAGAGGAC 120
Db |||||||
Qy 73833 GCCCAAACTGAGTACAACTTAAAGTACCTCTCTACCCCCAGTTCTTATGTGAGCCGAC 73892
Db |||||||
Qy 121 TCCTCCCAAGTGCAATTGCACAGGC-----TCACATGTCCTTTGCACATGGAACGCCACT 174
Db |||||||
Qy 73893 TCGCCCAAGTGTGACTGACTACCTTGACTTGAATGCTTTTTTGCACAGGAATAAAC 73952
Db |||||||
Qy 175 TCACCTTCAGTGTATCAACACAGCATGCAATTTGTGAGGAGAGTCAACGGAGGCCAAGT 234
Db |||||||
Qy 73953 GTCTCTCAGTATGACACACAGCATTCAGTTATTTGCAGA-AGGGAACCGAGGCCAAGT 74011
Db |||||||
Qy 235 GCTAAAGCCA-----CTGCGTTTGTCTTCTCCCTCCATTCAGGAACTCACAACTATGAGC 290
Db |||||||
Qy 74012 GATAAAGCCCAACCTTGTGTGTTCTCTCCCAATCCAGAACTCAGGACTGGAGCC 74071
Db |||||||
Qy 291 CTGTGGAGTTGCCAGTCTGATGAAGTTCAAAGTCTGGGCTGTTTTATACAATA--- 347
Db |||||||
Qy 74072 CATGTGTTTGCAA-----TTAAAGGCCAAAGTCTGACCTATTTTATAAACTATGA 74126
Db |||||||
Qy 348 -----AGCGCTGTGTGGCGTGGTATATCTTTTGAATTCAGCCTTTATGAGAAGC 399
Db |||||||
Qy 74127 CTGTGTTTATACATGTTTGGGTCGGTTCATTTTGGAGTCCATCTTTATGAATAGA 74186
Db |||||||
Qy 400 TGTACTATCTTTGTA--CCTGCTGAGGGCTGCTGGTCAGATGTGGGTGAACACCTGC 454
Db |||||||
Qy 74187 TAACCTGTCTTCTTAACCTGCTTGGATGGCTGGTAGTCAAATGTGAATGAACACCTAC 74243
Db |||||||
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Search completed: December 19, 2003, 14:06:16
Job time : 2134 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:39:44 ; Search time 256 Seconds
(without alignments)
5641.404 Million cell updates/sec

Title: US-09-620-607B-34
Perfect score: 535
Sequence: 1 gcagagacaaatgcccaaga.....aaaaatgttccttaactgg 535

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514.2	96.1	1040	24	ABL58680
2	514.2	96.1	1040	24	ABA96630
3	120	22.3	1737	23	AA591740
4	119.2	22.3	1737	23	AA591740
5	95.2	17.8	1020	24	ABA96621
6	95.2	17.8	1020	24	ABA96621
7	94	17.6	445	24	ABL61868
8	94	17.6	445	24	ABL61868
					Oesophagus cancer

9	87.8	16.4	465	24	ABL58672	Human X-type secre
10	87.8	16.4	465	24	ABA96622	Human X-type secre
11	63.4	11.9	65	24	ABN57123	Mouse spliced tran
12	36	6.7	758	23	AA567219	DNA encoding novel
13	36	6.7	758	23	AA584893	DNA encoding novel
14	35.4	6.6	830	20	AA335119	Human H19 promoter
15	35.4	6.6	830	21	AA72969	Human H19 promoter
16	35.4	6.6	830	22	AD21350	Human H19 promoter
17	35.4	6.6	3489	24	ABL62107	Colon adenocarcino
18	35.2	6.6	1830121	17	AA742063	Haemophilus influe
19	34.6	6.5	709	21	AA664439	Lycopersicon escul
20	34.6	6.5	709	21	AA664439	Lycopersicon escul
21	33.8	6.3	833	20	AA335520	Human H19 promoter
22	33.8	6.3	833	21	AA72970	Human H19 promoter
23	33.8	6.3	833	22	AD21351	Human H19 promoter
24	33.6	6.3	1204	24	ABK34913	Human CDNA encodin
25	33.6	6.3	26776	20	AA20254	Borrelia burgdorfe
26	33.4	6.2	1525	17	AA741945	ACC oxidase gene p
27	33.4	6.2	3681	20	AA05593	Nucleotide sequenc
28	33	6.2	5971	23	AA570348	DNA encoding novel
29	33	6.2	33718	22	AA65257	Human immune/haema
30	33	6.2	33718	22	AA65257	Human immune/haema
31	32.8	6.1	14041	22	AA86411	Internal control B
32	32.6	6.1	6836	24	AA45336	Human anti-microbi
33	32.6	6.1	659158	25	ABX16390	Mouse high growth
34	32.2	6.0	23580	22	AA528556	Genomic sequence #
35	32.2	6.0	23580	22	AA87248	Human immune/haema
36	32.2	6.0	86080	24	ABQ88164	Human osteoblast d
37	32.2	6.0	86080	24	ABQ88164	Human osteoblast d
38	32.2	6.0	580073	18	AA758840	Myocytoma genital
39	31.8	5.9	3655	23	ABL10552	Drosophila melanog
40	31.8	5.9	6467	24	ABN80169	Human chemically m
41	31.8	5.9	7616	23	ABL26746	Drosophila melanog
42	31.6	5.9	562	22	AAK37355	Human bone marrow
43	31.6	5.9	562	24	ABSL1341	Human genome-deriv
44	31.6	5.9	1125	24	ABK84533	Human CDNA differe
45	31.6	5.9	1125	24	ABL68131	Ovary cancer relat

ALIGNMENTS

RESULT 1
ABL58680
ID ABL58680 standard; DNA; 1040 BP.
XX
AC ABL58680;
XX
DT 27-AUG-2002 (first entry)
XX
DE Mouse X-type secretory phospholipase A2 encoding sequence.
XX
KW Mouse; X-type secretory phospholipase A2; X-type sPLA2; cancer; colon;
KW ovary; lung; stomach; kidney; gallbladder; prostate; spleen; testis;
KW liver; Alzheimer's disease; hepatocirrhosis; immunocaseay; gene; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 175..630
FT /tag= a
FT /product= "mouse X-type secretory phospholipase A2"

XX
PN WO200190196-A1.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-JP04267.
XX
PR 24-MAY-2000; 2000JP-0152967.
XX
PR 21-NOV-2000; 2000WO-JP08198.
XX
PA (SHIO) SHIONOGI & CO LTD.

Db 733 GCCACCTGGCTTTCCTTCCTCCATTCAGGAATCAACAATATGAGCTGTGGAGTT 792
 Qy 301 GCCAGTCTGATGAAGTTCAAGTCTGGGCTGTTTATACAAATAGCGCTGTGTGG 360
 Db 793 GCCAGTCTGATGAAGTTCAAGTCTGGGCTGTTTATACAAAT-AGCGCTGTGTGG 851
 Qy 361 GCGTGGTATACTTTTTCGAAATTCAGGCTTTATGAGAGCTGTACTATCTGTACCTGCTG 420
 Db 852 GCGTGGTATACTTTTTCGAAATTCAGGCTTTATGAGAGCTGTACTATCTGTACCTGCTG 911
 Qy 421 CAGGGCTGCTGGTCAGATGCGGTGAACACCTGCTAGGCTTTGCTGTGTAATAACATT 480
 Db 912 CAGGGCTGCTGGTCAGATGCGGTGAACACCTGCTAGGCTTTGCTGTGTAATAACATT 971
 Qy 481 GCCACATGATACATCTAAGAAATGTAACTGTAAATAAATAATGTTCCCTAA 531
 Db 972 GCCACATGATACATCTAAGAAATGTAACTGTAAATAAATAATGTTCCCTAA 1022

RESULT 3

AAX79001
 ID AAX79001 standard; cDNA; 742 BP.

XX AC AAX79001;
 XX DT 17-AUG-1999 (first entry)
 XX DE Human phospholipase A2 gene.
 XX KW Human; phospholipase A2; PHPLA2; ovarian tumour; antagonist; antibody;
 KW cancer; inflammation; ss.
 XX OS Homo sapiens.
 XX PN WO924587-A2.
 XX PD 20-MAY-1999.
 XX PP 04-NOV-1998; 98WO-US233555.
 XX PR 07-NOV-1997; 97US-0966317.
 XX PA (INCY-) INCYTE PHARM INC.
 XX PI Bandman O, Corley NC, Guegler KJ, Hawkins PR, Shah P;
 DR WPI; 1999-370674/31.
 DR P-PSDB; AAY07481.

PT New human phospholipase A2 protein useful for treating or preventing
 PT cancer or inflammation

PS Claim 7; Fig 1; 62pp; English.

CC This sequence represents the coding sequence for a novel 165 amino acid
 CC human phospholipase A2 (PHPLA2) protein. The sequence was isolated from
 CC clone 816403 from the human tumour cDNA library OVARUT01. Antagonists,
 CC e.g. antibodies, of PHPLA2 can be used to treat or prevent cancer or
 CC inflammation.

SQ Sequence 742 BP; 163 A; 216 C; 189 G; 173 T; 1 other;
 Query Match 22.4%; Score 120; DB 20; Length 742;
 Best Local Similarity 68.0%; Pred. No. 3.4e-30;
 Matches 215; Conservative 0; Mismatches 90; Indels 11; Gaps 3;

Qy 1 GCAGAGAACAAATGCCAAGACTTTTGTGAGGTGACAGAGCTGCTTACTGCTG 60
 Db 385 GCAGAGAACAAATGCCAAGACTTTTGTGAGGTGACAGAGCTGCTTACTGCTG 444
 Qy 61 GCAGGACCGGTACACCTGAATACCTCTTCTCCCTCCATTTATGTGAGAGGAC 120
 Db 445 GCCCAACTGAGTACAACTTAAGTACCTCTTCTTACCCCCCTTCTTATGTGAGCGGAC 504

Qy 121 TCTCCCAAGTGCAATTGACAGG-----TCATGTCCTTTGACATCGGAACGCACT 174
 Db 505 TCGCCCAAGTGTGACTGACTTACTTGTGAAATGCTCTTTTGCACAAGGAATAAAGC 564
 Qy 175 TCATTTTCAGTGTATCAACCAAGCATGCAATTTGTGCAGGAGAGTCCCGGAGGCCAAGT 234
 Db 565 GTCTCTCTCAGTAATGAACAACAGCATTCAGTTATTGTGCAGA-AGGGAACCGAAGCCAAGT 623
 Qy 235 GCTTAAGCCA-----CCTGGGTTTGTCTTCTCTTCATTTCAGGAATCAACTATGAGC 290
 Db 624 GATAAAGGCACAAACCTTGTGTTCCTCCCAATCCAGAACTCAGGACTGGAGCC 683
 Qy 291 CTGTGAGTTGCCAGT 306
 Db 684 CATGTAGTTTGCAGT 699

RESULT 4

AAS91740
 ID AAS91740 standard; cDNA; 1737 BP.

XX AC AAS91740;
 XX DT 13-FEB-2002 (first entry)
 XX DE DNA encoding novel human diagnostic protein #27544.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PP 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG27553.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS Claim 1; SEQ ID No 27544; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human

XX 24-MAY-2000; 2000JP-0152967.
 XX (SHIO) SHIONOGI & CO LTD.
 XX Hanasaki K, Imagawa K, Masuta K;
 XX WPI; 2002-097648/13.
 XX P-PSDB; AAM49001.
 XX Antibodies recognizing parts of X-type phospholipase A2 and their use
 XX in immunoassays for diagnosis of cancer and Alzheimer's disease -
 XX Disclosure; Page 40-41; 51pp; Japanese.
 XX The invention relates to antibodies which recognise parts of human X-type
 XX secretory phospholipase A2 (sPLA2; AAM49001, AAM49002). The antibodies of
 XX the invention are specific for the N-terminal propeptide sequence (Glu
 XX -11 to Arg -1) or for the active enzyme (Gly 1 to Asp 123). The invention
 XX also relates to a method of assaying for the X-type sPLA2 propeptide or
 XX active enzyme, and a method for the diagnosis of X-type sPLA2-associated
 XX diseases using the assay. The differing specificities of the antibodies
 XX allows determination of the relative amounts of proenzyme and active
 XX enzyme present. The invention also encompasses drug compositions which
 XX contain antibodies to the sPLA2 active enzyme for the treatment of
 XX X-type sPLA2-associated diseases. The antibodies are used for the
 XX diagnosis and treatment of X-type sPLA2-associated diseases including
 XX cancer of the colon, lung, liver, stomach, kidney, gall bladder, prostate
 XX and pancreas, Alzheimer's disease and liver cirrhosis. The present
 XX sequence is a DNA encoding a 165 residue human X-type sPLA2.
 XX Sequence 1020 BP; 212 A; 304 C; 291 G; 213 T; 0 other;
 XX
 XX Query Match 17.8%; Score 95.2; DB 24; Length 1020;
 XX Best Local Similarity 69.5%; Pred. No. 1.2e-21;
 XX Matches 146; Conservative 0; Mismatches 58; Indels 6; Gaps 1;
 XX
 XX 1 GCAGAGAACAAATGCCAAGACTTTTGTGCGAGGTGACGAGGAGCTGCTTACTGCTG 60
 XX 801 GCAGAGAACAAATGCCAAGACTTTTGTGCGAGGTGACGAGGAGCTGCTTACTGCTT 860
 XX 61 GCAGGACCGAGTACCACTGAATACCTCTCTTCCCTCCCTCCATTTTATGTGAGAGGAC 120
 XX 861 GCCCAACTGAGTACAACTTAAGTACTCTCTTACCCCGAGTCTTATGTGAGCGGAC 920
 XX 121 TCTCCCAAGTGCATTCACAGGC-----TCACATGTCCCTTTGCACATGGAACGCACT 174
 XX 921 TCGCCCAAGTGTGACTGACTTACCTTGTGACTTGAATGCTCTTTGCACAGGAATAAAGC 980
 XX 175 TCACCTTCAGTATCACCACAGCATGCAA 204
 XX 981 GTCTCTCTCAGTAATGAAAAA 1010
 XX
 XX RESULT 7
 XX ABL61868/c
 XX ID ABL61868 standard; DNA; 445 BP.
 XX
 XX AC ABL61868;
 XX XX
 XX 15-MAY-2002 (first entry)
 XX
 XX Colon adenocarcinoma related gene sequence SEQ ID NO:205.
 XX
 XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 XX cytostatic; Gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
 XX Gene; ds.
 XX
 XX Homo sapiens.
 XX OS
 XX WO200194629-A2.
 XX PN
 XX

PD 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US10838.

XX 05-JUN-2000; 2000US-209473P.

XX 05-JUN-2000; 2000US-209531P.

XX 18-SEP-2000; 2000US-233133P.

XX 18-SEP-2000; 2000US-233617P.

XX 20-SEP-2000; 2000US-234009P.

XX 20-SEP-2000; 2000US-234034P.

XX 20-SEP-2000; 2000US-234052P.

XX 22-SEP-2000; 2000US-234509P.

XX 22-SEP-2000; 2000US-234567P.

XX 25-SEP-2000; 2000US-234923P.

XX 25-SEP-2000; 2000US-234924P.

XX 25-SEP-2000; 2000US-235077P.

XX 25-SEP-2000; 2000US-235082P.

XX 25-SEP-2000; 2000US-235134P.

XX 25-SEP-2000; 2000US-235134P.

XX 26-SEP-2000; 2000US-235637P.

XX 26-SEP-2000; 2000US-235638P.

XX 27-SEP-2000; 2000US-235711P.

XX 27-SEP-2000; 2000US-235720P.

XX 27-SEP-2000; 2000US-235840P.

XX 27-SEP-2000; 2000US-235863P.

XX 28-SEP-2000; 2000US-236028P.

XX 28-SEP-2000; 2000US-236032P.

XX 28-SEP-2000; 2000US-236033P.

XX 28-SEP-2000; 2000US-236034P.

XX 28-SEP-2000; 2000US-236109P.

XX 28-SEP-2000; 2000US-236111P.

XX 29-SEP-2000; 2000US-236842P.

XX 29-SEP-2000; 2000US-236891P.

XX 02-OCT-2000; 2000US-237172P.

XX 02-OCT-2000; 2000US-237173P.

XX 02-OCT-2000; 2000US-237278P.

XX 02-OCT-2000; 2000US-237294P.

XX 02-OCT-2000; 2000US-237295P.

XX 02-OCT-2000; 2000US-237316P.

XX 03-OCT-2000; 2000US-237425P.

XX 03-OCT-2000; 2000US-237598P.

XX 03-OCT-2000; 2000US-237604P.

XX 03-OCT-2000; 2000US-237606P.

XX 03-OCT-2000; 2000US-237608P.

XX 01-NOV-2000; 2000US-244867P.

XX 01-NOV-2000; 2000US-245084P.

XX (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 XX Soppet DR, Weaver Z;
 XX WPI; 2002-188264/24.XX Screening for anti-neoplastic agent involves exposing cells to a
 XX chemical agent to be tested for anti-neoplastic activity, and
 XX determining a change in expression of a gene of a signature gene set

XX Claim 1; SEQ ID 205; 44pp; English.

XX The present invention describes a method (M1) for screening for an
 XX anti-neoplastic agent. The method involves exposing cells to a chemical
 XX agent to be tested for anti-neoplastic activity, determining a change in
 XX expression of at least one gene (I) of a signature gene set, where (I)
 XX comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 XX to ABL70110), or is at least 95% identical to (S), where a change in
 XX expression is indicative of anti-neoplastic activity. (I) has cytostatic
 XX activity and can be used in gene therapy. M1 can be used for screening
 XX an anti-neoplastic agent, and can be used for producing a product which
 XX is the data collected with respect to the anti-neoplastic agent as a
 XX result of M1, and the data is sufficient to convey the chemical
 XX structure and/or properties of the agent. M1 can be used in the
 XX treatment of cancer such as colon, breast, stomach, lung, thyroid,

CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.
 XX
 SQ Sequence 445 BP; 99 A; 118 C; 120 G; 106 T; 2 other;
 Query Match 17.6%; Score 94; DB 24; Length 445;
 Best Local Similarity 71.4%; Pred. No. 2e-21;
 Matches 140; Conservative 0; Mismatches 50; Indels 6; Gaps 1;
 Qy 1 GCAGAGAACAAATGCCAGAGACTTTGTGCGAGGTGTGACGAGGAGCTTACTGCTG 60
 Db 199 GCAGAGAACAAATGCCAGAGACTTTGTGCGAGGTGTGACGAGGAGTTCCTAACTGCTTA 140
 Qy 61 GCAGGAGCCGAGTACCACTTGTGCGAGGTGTGACGAGGAGCTTACTGCTG 60
 Db 199 GCAGAGAACAAATGCCAGAGACTTTGTGCGAGGTGTGACGAGGAGTTCCTAACTGCTTA 140
 Qy 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGTCCTTTGCACATGGAAGGCACT 174
 Db 79 TCGCCCAAGTGTGACTGACTACCTTGACTTGAAATGCTCTTTGCACAAAGGAATAAAGC 20
 Qy 175 TCACATTCAGTGATCA 190
 Db 19 GTCCTCTCAGTAATGA 4
 RESULT 8
 ABL67612/c
 ID ABL67612 standard; DNA; 445 BP.
 XX
 AC ABL67612;
 DT 15-MAY-2002 (first entry)
 XX
 DE Oesophagus cancer related gene sequence SEQ ID NO:5949.
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cystostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 XN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PP 30-MAY-2001; 2001WO-US10838.
 XX
 PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.

PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 29-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237315P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX
 PA (AVAL-) AVALON PHARM.
 XX
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 XX WPI; 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set
 XX
 XX Claim 1; SEQ ID 5949; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.
 XX
 SQ Sequence 445 BP; 99 A; 118 C; 120 G; 106 T; 2 other;
 Query Match 17.6%; Score 94; DB 24; Length 445;
 Best Local Similarity 71.4%; Pred. No. 2e-21;
 Matches 140; Conservative 0; Mismatches 50; Indels 6; Gaps 1;
 Qy 1 GCAGAGAACAAATGCCAGAGACTTTGTGCGAGGTGTGACGAGGAGCTTACTGCTG 60
 Db 199 GCAGAGAACAAATGCCAGAGACTTTGTGCGAGGTGTGACGAGGAGTTCCTAACTGCTTA 140
 Qy 61 GCAGGAGCCGAGTACCACTTGTGCGAGGTGTGACGAGGAGCTTACTGCTG 120
 Db 139 GCCCAACTGAGTACAACTTAAAGTACCTCTTCTACCCCGAGTTCCTATGTGAGCCGAC 80
 Qy 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGTCCTTTGCACATGGAAGGCACT 174
 Db 79 TCGCCCAAGTGTGACTGACTACCTTGACTTGAAATGCTCTTTGCACAAAGGAATAAAGC 20
 Qy 175 TCACATTCAGTGATCA 190
 Db 19 GTCCTCTCAGTAATGA 4

RESULT 9
 ABL58672
 ID ABL58672 standard; DNA; 465 BP.
 AC ABL58672;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human X-type secretory phospholipase A2 encoding sequence.
 XX
 KW Human; X-type secretory phospholipase A2; X-type sPLA2; cancer; colon;
 KW liver; lung; stomach; kidney; gallbladder; prostate; spleen; testis;
 KW ovary; Alzheimer's disease; hepatocirrhosis; immunoassay; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..465
 FT /tag= a
 FT /partial
 FT /product= "human X-type secretory phospholipase A2"
 FT /note= "no stop codon present"
 FT sig_peptide 1..96
 FT /tag= b
 FT mat_peptide 97..465
 FT /tag= c
 XX
 PN WO200190196-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 22-MAY-2001; 2001WO-JP04267.
 XX
 PR 24-MAY-2000; 2000JP-0152967.
 PR 21-NOV-2000; 2000WO-JP08198.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 PI Hanasaki K, Imagawa K, Masuta K;
 DR WPI: 2002-404351/43.
 DR P-PSDB; ABB80081.
 XX
 PT Immunoassay of X-type phospholipase A2 with antibody recognising part
 PT of it for quantitation of activated version, useful in diagnosis of
 PT e.g. cancer of colon, prostate, ovary or spleen, Alzheimer's disease
 PT and hepatocirrhosis
 XX
 PS Claim 1; Page 50; 59pp; Japanese.
 XX
 CC The invention relates to an antibody that can specifically recognise a
 CC part of X-type secretory phospholipase A2 (X-type sPLA2). The immunoassay
 CC of the invention is used in the diagnosis of e.g. cancer of the colon,
 CC liver, lung, stomach, kidney, gallbladder, prostate, spleen, testis or
 CC ovary, Alzheimer's disease and hepatocirrhosis. The current sequence
 CC represents a human X-type secretory phospholipase A2 encoding sequence.
 XX
 SQ Sequence 465 BP; 90 A; 136 C; 134 G; 105 T; 0 other;
 Query Match 16.4%; Score 87.8; DB 24; Length 465;
 Best Local Similarity 79.4%; Pred. No. 2.7e-19;
 Matches 104; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 QY 1 GCAGGACCAATGCCAAGACTTTTGTGCGAGTGTGACGAGGAGTGGCTACTGCTG 60
 DB 331 GCAGGACCAATGCCAAGACTTTTGTGCGAGTGTGACGAGGAGTGGCTACTGCTTA 390
 QY 61 GCAGGACGAGTACCACCTGAATACCTCTTCTCCCTCCATTTATGTGAGGAGGAC 120
 DB 391 GCCCAACTGAGTACACTTAAGTACCTCTTCTACCCCGATTCTCTAATGAGCCGAC 450

QY 121 TCTCCCAAGTG 131
 DB 451 TCGCCCAAGTG 461
 RESULT 10
 ABA96622
 ID ABA96622 standard; DNA; 465 BP.
 XX
 AC ABA96622;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human X-type secretory phospholipase A2 (sPLA2) DNA, SEQ ID NO:3.
 XX
 KW Human; X-type; secretory phospholipase A2; sPLA2; immunoassay;
 KW cancer; tumour; colon; lung; liver; stomach; kidney; gall bladder;
 KW prostate; pancreas; Alzheimer's disease; liver cirrhosis; cytostatic;
 KW neutropic; neuroprotective; hepatotropic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..465
 FT /tag= a
 FT /partial
 FT /product= "Human X-type sPLA2 precursor"
 FT /note= "No stop codon given"
 FT sig_peptide 1..96
 FT /tag= b
 FT mat_peptide 97..465
 FT /tag= c
 FT /product= "Active human X-type sPLA2"
 XX
 PN WO200190195-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 21-NOV-2000; 2000WO-JP08198.
 XX
 PR 24-MAY-2000; 2000JP-0152967.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 PI Hanasaki K, Imagawa K, Masuta K;
 DR WPI: 2002-097648/13.
 DR P-PSDB; ABA9002.
 XX
 PT Antibodies recognizing parts of X-type phospholipase A2 and their use
 PT in immunoassays for diagnosis of cancer and Alzheimer's disease -
 XX
 PS Claim 1; Page 42-43; 51pp; Japanese.
 XX
 CC The invention relates to antibodies which recognise parts of human X-type
 CC secretory phospholipase A2 (sPLA2; ABA9001, ABA9002). The antibodies of
 CC the invention are specific for the N-terminal propeptide sequence (Glu
 CC -11 to Arg -1) or for the active enzyme (Gly 1 to Asp 123). The invention
 CC also relates to a method of assaying for the X-type sPLA2 propeptide or
 CC active enzyme, and a method for the diagnosis of X-type sPLA2-associated
 CC diseases using the assay. The differing specificities of the antibodies
 CC allows determination of the relative amounts of proenzyme and active
 CC enzyme present. The invention also encompasses drug compositions which
 CC contain antibodies to the sPLA2 active enzyme for the treatment of
 CC X-type sPLA2-associated diseases. The antibodies are used for the
 CC diagnosis and treatment of X-type sPLA2-associated diseases including
 CC cancer of the colon, lung, liver, stomach, kidney, gall bladder, prostate
 CC and pancreas, Alzheimer's disease and liver cirrhosis. The present
 CC sequence is a DNA encoding a 155 residue human X-type sPLA2.
 XX
 SQ Sequence 465 BP; 90 A; 136 C; 134 G; 105 T; 0 other;
 Query Match 16.4%; Score 87.8; DB 24; Length 465;

Best Local Similarity 79.4%; Pred. No. 2.7e-19;
Matches 104; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GCAGAGACAAATGCCAAGACTTTTGTGACAGTGTGACGAGAGCTGGCTTACTGCCTG 60
DB |||||
331 GCAGAGACAAATGCCAAGACTTTTGTGACAGTGTGACGAGAGCTGGCTTACTGCCTTA 390
QY 61 GCAGGACCGAGTACCACCTGAATACCTTTCTTCCCTCCATTATGTGAGAGGAC 120
DB |||||
391 GCCCAAACTGAGTACAACTTAAAGTACTCTTCTACCCCACTCTCTATGTGAGCGGAC 450
QY 121 TCTCCCAAGTG 131
DB |||||
451 TCGCCCAAGTG 461

RESULT 11

ABN57123
ID ABN57123 standard; DNA; 65 BP.

XX AC ABN57123;

DT 15-JUL-2002 (first entry)

XX DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:29871.

XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;

XX KW splice variant; transcriptome; oligonucleotide library; ss.

XX OS Mus musculus.

XX PN WO200210449-A2.

XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-IB01903.

XX PR 28-JUL-2000; 2000US-221607P.

XX PR 02-MAY-2001; 2001US-287724P.

XX PA (COMP-)-COMPUGEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI; 2002-257383/30.

XX PT New oligonucleotide libraries comprising oligonucleotides which
selectively hybridize to mRNAs transcribed from a transcription unit of
a genome, useful for detecting tissue-, pathology-, and
developmental-specific genes -

XX PS Example 1; SEQ ID 29871; 47pp; English.

XX CC The present invention describes oligonucleotide libraries for detecting
messenger RNAs that populate a (sub-)transcriptome, where the
(sub-)transcriptome comprises messenger RNAs transcribed from multiple
transcription units that populate a genome. The library comprises
several oligonucleotides, each capable of hybridizing selectively to a
set of messenger RNAs transcribed from a given transcription unit of
the genome, which encodes one or more messenger RNA splice variants.
The oligonucleotide libraries are useful for detecting mRNAs from a
biological sample, in expression profiling studies, in qualitatively or
quantitatively characterizing the corresponding transcriptome, and in
detecting RNA transcripts and splice variants of human or animal
transcriptomes. The libraries may also be used as specialised mini
libraries to detect transcripts of a sub-transcriptome under a
particular biological or pathological state, and so allowing the
detection of tissue- and pathology-specific genes such as those genes
only expressed in specific tissue under a specific pathological
condition; to detect developmental specific genes; and to detect RNA
transcripts and splice variants of a transcriptome; of a patient suffering
from a particular disorder. ABN27253 to ABN59589 represent
oligonucleotide sequences from rats, humans and mice, which are used in

CC the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 65 BP; 12 A; 13 C; 22 G; 18 T; 0 other;

Query Match 11.9%; Score 63.4; DB 24; Length 65;

Best Local Similarity 98.5%; Pred. No. 2e-11;

Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 412 TACCTGCTGCAGGGCTGCTGCTCAGATGGGTGACACCTCTTAGGCTTGCTGTGT 471

DB 1 TACCTGCTGCAGGGCTGCTGCTCAGATGGGTGACACCTCTTAGGCTTGCTGTGT 60

QY 472 AATAA 476

DB 61 AATAA 65

RESULT 12

AAS67219/c

ID AAS67219 standard; cDNA; 758 BP.

XX AC AAS67219;

DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #3023.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Dmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG03032.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity -

XX PS Claim 1; SEQ ID NO 3023; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and
polypeptide (II) sequences. (I) is useful as hybridisation probes,
polymerase chain reaction (PCR) primers, oligomers, and for chromosome
and gene mapping, and in recombinant production of (II). The
polynucleotides are also used in diagnostics as expressed sequence tags
for identifying expressed genes. (I) is useful in gene therapy techniques
to restore normal activity of (II) or to treat disease states involving
(II). (II) is useful for generating antibodies against it, detecting or
quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (II) and its binding partners are useful in medical
imaging of sites expressing (II). (I) and (II) are useful for treating
disorders involving aberrant protein expression or biological activity.
The polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 758 BP; 154 A; 179 C; 263 G; 155 T; 7 other;
 Query Match 6.7%; Score 36; DB 23; Length 758;
 Best Local Similarity 51.3%; Pred. No. 0.18;
 Matches 81; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
 QY 5 AGAACAAATGCCAAGAACTTTTGTGAGGTGTGACGAGGAGCTGGCTTACTGCTGGCAG 64
 DB 567 AGGACTGGTNCCTCACTCTGAAGAGGTAAACGGGTGCGNAGGCGCACCGGTGCCCT 508
 QY 65 GGACCGAGTACCACTGAAATACCTCTTCTCCCTCCATTTTATCTGAGAGGACTCTC 124
 DB 507 GCTCCTGTCTACAACTTGTGCGGACCAACGACTCCCAATCTTAGATAAGGTGATCTTGC 448
 QY 125 CCAAGTGCATTTGACAGGCTCACATGTCCCTTTGCACA 162
 DB 447 CCAGCTGACGAGGCTTGGACACTTGGCGGCTCCAGA 410
 RESULT 13
 ID AAS84693/c
 XX AAS84693 standard; cDNA; 758 BP.
 AC AAS84693;
 XX
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #20497.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.
 OS
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG20506.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1; SEQ ID No 20497; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 758 BP; 154 A; 179 C; 263 G; 155 T; 7 other;
 Query Match 6.7%; Score 36; DB 23; Length 758;
 Best Local Similarity 51.3%; Pred. No. 0.18;
 Matches 81; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
 QY 5 AGAACAAATGCCAAGAACTTTTGTGAGGTGTGACGAGGAGCTGGCTTACTGCTGGCAG 64
 DB 567 AGGACTGGTNCCTCACTCTGAAGAGGTAAACGGGTGCGNAGGCGCACCGGTGCCCT 508
 QY 65 GGACCGAGTACCACTGAAATACCTCTTCTCCCTCCATTTTATCTGAGAGGACTCTC 124
 DB 507 GCTCCTGTCTACAACTTGTGCGGACCAACGACTCCCAATCTTAGATAAGGTGATCTTGC 448
 QY 125 CCAAGTGCATTTGACAGGCTCACATGTCCCTTTGCACA 162
 DB 447 CCAGCTGACGAGGCTTGGACACTTGGCGGCTCCAGA 410
 RESULT 14
 ID AAX33519/c
 XX AAX33519 standard; DNA; 830 BP.
 AC AAX33519;
 XX
 DT 07-JUL-1999 (first entry)
 DE Human H19 promoter sequence SEQ ID NO:1.
 XX Human; H19; promoter; enhancer; tumour; cytotoxicity; carcinoma; cancer;
 KW IGF promoter; insulin like growth factor; hepatoblastoma; astrocytoma;
 KW rhabdomyosarcoma; ganglioblastoma; neuroblastoma; ss.
 XX Homo sapiens.
 OS
 PN WO9918195-A2.
 XX
 PD 15-APR-1999.
 XX
 PF 04-OCT-1998; 98WO-IL00486.
 XX
 PR 03-OCT-1997; 97US-0943608.
 XX
 PA (YISS) YISSUM RES & DEV CO.
 XX
 PI Ayesh S, Hochberg A;
 XX
 DR WPI; 1999-264016/22.
 XX
 PT Expressing heterologous cytotoxic agent selectively in tumour cells
 PS Claim 13; Page 63; 68pp; English.
 CC The present invention describes genes encoding cytotoxic products which
 CC are expressed in cancer cells under the control of regulatory
 CC transcriptional sequences. Also described are: (i) a method for
 CC transcribing a heterologous sequence (I), encoding a cytotoxic product, in
 CC a tumour cell comprising introducing a polynucleotide (A) comprising (i)
 CC linked to regulatory sequences that are: (a) derived from a genomically
 CC imprinted gene (ii) that is expressed specifically in tumour cells, or

CC (b) is the IGF (insulin-like growth factor)-1 promoter. (2) vectors
CC containing (A); and (3) host cells containing the vector of (2). (A) are
CC used in gene therapy of a wide range of cancers, particularly carcinoma
CC (of bladder, liver, ovary, cervix, lung, breast, oesophagus, thyroid, or
CC squamous cell carcinoma of head and neck); hepatoblastoma;
CC rhabdomyosarcoma; astrocytoma; ganglioblastoma and neuroblastoma. The
CC specified regulators provide tumour-specific expression. The present
CC sequence represents a specifically claimed human H19 promoter sequence
CC from the present invention.

XX
SQ Sequence 830 BP; 151 A; 245 C; 312 G; 122 T; 0 other;

Query Match 6.6%; Score 35.4; DB 20; Length 830;
Best Local Similarity 55.2%; Pred. No. 0.3;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 70 GAGTACCACTGAATACCTCTCTTCCCTCCATTTATGTGAGAGGACTCTCCCAAG 129
DB 796 GTGGCCCGCAGATTCCCGCCCTGCGCCCAATCAGAGGAGGCGCTCCCGAG 737

QY 130 TGAATTGACAGGCTCACATGTCCTTTTGACATGGAAACGCACTTCATTTTCAGTGATC 189
DB 736 GGCCCGCGCAGGCGCCACCTCCGCTGGAGAGTTCAGACACACAGTCTCTCTCACCAGC 677

QY 190 ACCAA 194
DB 676 ACCCA 672

RESULT 15

AAA72969/C

ID AAA72969 standard; DNA; 830 BP.

XX AC AAA72969;

XX DT 23-NOV-2000 (first entry)

XX DE Human H19 promoter nucleotide sequence SEQ ID NO:1.

XX KW Human; H19 promoter; H19 enhancer; expression; cytotoxic; tumour;

XX KW transcription; regulation; cancer; cytostatic; gene therapy; ds.

XX OS Homo sapiens.

XX PN US6087164-A.

XX PD 11-JUL-2000.

XX PF 01-OCT-1998; 98US-0165240.

XX PR 03-OCT-1997; 97US-0943608.

XX PA (YISS) YISSUM RES & DEV CO.

XX PI Ayesh S, Hochberg A;

XX DR WPI; 2000-531346/48.

XX PT Expression of heterologous sequences especially genes encoding

XX PT cytotoxic products in tumor cells for treating cancer, by transforming

XX PT tumor cells with heterologous sequence linked with a regulatory

XX PT sequence -

XX PS Claim 4; Fig 1A-C; 33pp; English.

XX PS The present invention describes a method for expressing a heterologous

XX CC sequence in a tumour cell. The method comprises introducing into the

XX CC tumour cell a polynucleotide (1) comprising a regulatory sequence

XX CC operably linked to a heterologous sequence encoding a cytotoxic gene

XX CC product, where the regulatory sequence is derived from a genomically

XX CC imprinted gene that is specifically expressed in the tumour cell. The

XX CC present sequence represents a specifically claimed human H19 promoter

XX CC nucleotide sequence use in the method of the invention. The method is

CC useful for selective expression of heterologous genes in tumour cells
CC in a subject having bladder, hepatocellular, ovarian, cervical, lung
CC or breast carcinoma, squamous cell carcinoma in head and neck,
CC oesophageal and thyroid carcinoma, astrocytoma, ganglioblastoma,
CC neuroblastoma, hepatoblastoma or rhabdomyosarcoma. This method is useful
CC for treating wide variety of cancers and hyperproliferative conditions.
CC The method can be used in gene therapy techniques.

XX
SQ Sequence 830 BP; 151 A; 245 C; 312 G; 122 T; 0 other;

Query Match 6.6%; Score 35.4; DB 21; Length 830;
Best Local Similarity 55.2%; Pred. No. 0.3;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 70 GAGTACCACTGAATACCTCTCTTCCCTCCATTTATGTGAGAGGACTCTCCCAAG 129
DB 796 GTGGCCCGCAGATTCCCGCCCTGCGCCCAATCAGAGGAGGCGCTCCCGAG 737

QY 130 TGAATTGACAGGCTCACATGTCCTTTTGACATGGAAACGCACTTCATTTTCAGTGATC 189
DB 736 GGCCCGCGCAGGCGCCACCTCCGCTGGAGAGTTCAGACACACAGTCTCTCTCACCAGC 677

QY 190 ACCAA 194
DB 676 ACCCA 672

Search completed: December 19, 2003, 13:30:33

Job time : 260 secs

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:39:44 ; Search time 2067 Seconds
(without alignments)
6290.709 Million cell updates/sec

Title: US-09-620-607b-34

Perfect score: 535

Sequence: 1 gcagagacaaatgcccaaga.....aaaaaatgtccctaactgg 535

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_esthc.*

9: gb_estl.*

10: gb_estc2.*

11: gb_estc3.*

12: gb_estc4.*

13: gb_estc5.*

14: gb_estfun.*

15: em_estom.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vit.*

21: em_gss_fun.*

22: em_gss_man.*

23: em_gss_mus.*

24: em_gss_pto.*

25: em_gss_rod.*

26: em_gss_pmg.*

27: em_gss_vrl.*

28: gb_ges1.*

29: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520.4	97.3	611	10 BB015940	BB015940 BB015940
2	520.4	97.3	823	11 AK076921	AK076921 Mus muscu
3	458.4	85.7	486	4 BX528749	BX528749 RZPD Mus
4	453.6	84.8	480	9 AA611431	AA611431 v051909.r

5	382.8	71.6	408	9	AA607557	AA607557 vo44d05.r
6	371.6	69.5	834	12	BG964576	BG964576 602833255
7	297	55.5	587	10	BB615766	BB615766 BB615766
8	284.4	53.2	322	10	BB548845	BB548845 BB548845
9	284	53.1	311	9	AV053175	AV053175 AV053175
10	270.6	50.6	314	9	AV075661	AV075661 AV075661
11	266.4	49.8	288	9	AV081069	AV081069 AV081069
12	260.8	48.7	497	9	AA851843	AA851843 EST194611
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16	213.8	40.0	245	10	BB535230	BB535230 BB535230
17	199.2	37.2	225	9	AV079620	AV079620 AV079620
18	196.6	36.7	239	9	AV370437	AV370437 AV370437
19	196.2	36.7	238	9	AV370433	AV370433 AV370433
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ALIGNMENTS

RESULT	1	611 bp	linear	EST 18-OCT-2001
BB015940	BB015940	RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930556P12 3', similar to AFI66097 Mus musculus group X secreted phospholipase A2 (Pla2g10), mRNA sequence.		
LOCUS	BB015940			
DEFINITION	BB015940			
ACCESSION	BB015940			
VERSION	BB015940.2	GI:16257430		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
AUTHORS	1 (bases 1 to 611)			
	Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, P., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.			
TITLE	RIKEN Mouse ESTs (Arakawa, T., et al. 2001)			
JOURNAL	Unpublished			
COMMENT	On Jun 2, 2000 this sequence version replaced gi:8186926. Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute			

79 GCAGAGAACAAATGCCAAGACCTTTTGTGCAGGTGTGACGAGAGCTGGCTTACTGCCTG 138

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199 TCTCCCAAGTGCATTTGACAGGCTCACATGTCCTTTGACATGGAAGCGCACTTCACATT 258

181 TCAGTGATCACCAACAGCATGCAATTTGTGCAGGAGAGTCACTGGAGGCGCAAGTGTCTAAA 240

259 TCAGTGATCACCAACAGCATGCAATTTGTGCAGGAGAGTCACTGGAGGCGCAAGTGTCTAAA 318

241 GCCACTGCGTTTGTCTTCTTCCATTCAGAACTCAACTATGAGCCTGTGAGATT 300

319 GCCACTGCGTTTGTCTTCTTCCATTCAGAACTCAACTATGAGCCTGTGAGATT 378

301 GCCAGTCTGATCAAGGTTCCAAAGTCTCTGGGCTGTTTTATACAAATAAGCGCTGTGTGG 360

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RESULT 2

AK076921

LOCUS

DEFINITION

Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930556P12 product:phospholipase A2, group X, full insert sequence.

AK076921.1 GI:26345757

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Carninci, P., Shibata, Y., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Konno, H., Akiyama, J., Nishikawa, S., Hazama, M., Nishine, T., Harada, A., Sumi, N., Ishii, Y., Nakamura, S., Sakaguchi, S., Ikegami, F., Kashiwagi, K., Yamamoto, R., Matsumoto, H., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K., Fujiwara, S., Inoue, K., Tanaka, T., Tanaka, T., Matsura, S., Kawai, J., Yoneda, Y., Ishikawa, T., Ozawa, K., Kira, A. and Hayashizaki, Y. OKAZAKI, Y., MURAMATSU, M., INOUE, Y., KIRA, A. and HAYASHIZAKI, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

4

AK076921

LOCUS

DEFINITION

Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930556P12 product:phospholipase A2, group X, full insert sequence.

AK076921.1 GI:26345757

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

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Carninci, P., Shibata, Y., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Konno, H., Akiyama, J., Nishikawa, S., Hazama, M., Nishine, T., Harada, A., Sumi, N., Ishii, Y., Nakamura, S., Sakaguchi, S., Ikegami, F., Kashiwagi, K., Yamamoto, R., Matsumoto, H., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K., Fujiwara, S., Inoue, K., Tanaka, T., Tanaka, T., Matsura, S., Kawai, J., Yoneda, Y., Ishikawa, T., Ozawa, K., Kira, A. and Hayashizaki, Y. OKAZAKI, Y., MURAMATSU, M., INOUE, Y., KIRA, A. and HAYASHIZAKI, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

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MEDLINE
PUBMED
REFERENCE
AUTHORS
20530913
11076861
4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
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and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 823)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tegawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.
FEATURES
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RESULT 3

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AV081063
LOCUS
DEFINITION

[illegible]

AV081069
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 Mus musculus (house mouse)
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 1 (bases 1 to 288)
 Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, P., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsu, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 RIKEN Mouse ESTs
 Unpublished
 Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@tc.riken.go.jp
 Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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 1 (bases 1 to 497)
 Lee, N.H., Glodok, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
 Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
 Unpublished
 Contact: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
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LOCUS BB552490
DEFINITION BB552490 RIKEN full-length enriched, 2 days pregnant adult female
OVIDUCT Mus musculus cDNA clone E230038E12 3', similar to AF166097
Mus musculus group X secreted phospholipase A2 (Pla2g10) mRNA, mRNA
sequence.
ACCSSION BB552490 325 bp mRNA linear EST 01-AUG-2000
VERSION BB552490
KEYWORDS BB552490
SOURCE BB552490.1 GI:9638856
ORGANISM Mus musculus (house mouse)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 325)
TITLE Endo, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
JOURNAL Iizawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
COMMENT Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y.,
Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Toninaga, N., Toya,
T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino,
M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagasaka, S., Sasaki,
N., Okazaki, Y., Muramatsu, Y., and Hayashizaki, Y.
Thermotabilization and thermoactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitzunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y., and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES
source
1..325
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="E230038E12"
/sex="female"
/tissue_type="oviduct"
/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 2 days pregnant
adult female oviduct"
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGCGCGCCGCACTCGAGTTTCTTTTCTTTT 3'], cDNA was

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:39:44 ; Search time 78 Seconds
(without alignments)
3027.436 Million cell updates/sec

Title: US-09-620-607B-34

Perfect score: 535
Sequence: 1 gcagagaaatgccaaga.....aaaaatgtccctaactgg 535

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	22.4	742	3	US-08-966-317-2
2	120	22.4	742	4	US-09-489-770-2
3	35.4	6.6	830	3	US-09-165-240-1
4	35.4	6.6	830	4	US-09-568-059-1
5	35.2	6.6	1830121	4	US-09-557-884-1
6	35.2	6.6	1830121	4	US-09-643-990A-1
7	33.8	6.3	833	3	US-09-165-240-2
8	33.8	6.3	833	4	US-09-568-059-2
9	33.4	6.2	1925	3	US-08-894-324A-1
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27	29.2	5.5	3815	4	US-08-936-165A-196

28	29.2	5.5	6573	4	US-09-252-991A-9183
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45	28.4	5.3	4655	4	US-09-207-914-20

ALIGNMENTS

RESULT 1
US-08-966-317-2
; Sequence 2, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,317
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVARUT01
CLONE: 816403
US-08-966-317-2

Query Match 22.4%; Score 120; DB 3; Length 742;
Best Local Similarity 68.0%; Pred. No. 8.6e-31;


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RESULT 2
US-09-489-770-2
; Sequence 2, Application US/09489770
; Patent No. 6399301
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,770
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/966,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 742 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVARUT01
; CLONE: 816403

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Db 684 CATGTAGTTTGCAGT 699

Query Match 22.4%; Score 120; DB 4; Length 742;
Best Local Similarity 68.0%; Pred. No. 8.6e-31;
Matches 215; Conservative 0; Mismatches 90; Indels 11; Gaps 3;
QY 1 GCAGAGAACAAATCCCAAGAACTTTTGTGCAAGTGTGACGAGGAGCTGGCTTACTGCTG 60
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RESULT 3
US-09-165-240-1/c
; Sequence 1, Application US/09165240A
; Patent No. 6087164
; GENERAL INFORMATION:
; APPLICANT: Hochberg, Abraham
; APPLICANT: Ayeshe, Suhail
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
; FILE REFERENCE: 9457-0014-999
; CURRENT APPLICATION NUMBER: US/09/165,240A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: US 08/943,608
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-165-240-1

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Best Local Similarity 55.2%; Pred. No. 0.053;
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QY 190 ACCAA 194
Db 676 ACCCA 672

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; Sequence 1, Application US/09568059
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; Patent No. 6306833
; GENERAL INFORMATION:
; APPLICANT: Hochberg, Abraham
; APPLICANT: Ayesh, Suhail
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
; FILE REFERENCE: 9457-0014-999
; CURRENT APPLICATION NUMBER: US/09/568,059
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/165,240
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-568-059-1

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Best Local Similarity 55.2%; Pred. No. 0.053;
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Qy 190 ACCAA 194
Db 676 ACCCA 672

RESULT 5
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match          6.6%; Score 35.2; DB 4; Length 1830121;
Best Local Similarity 49.5%; Pred. No. 4.7;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

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Db 1392777 GAAATTTTATCCATGCAAGAACGGCTTGCCTCATCATGATTCTTTGAATATATTTT 1392718

Qy 261 CTTTCCATTCAGGAACCTCACAACTATGAGCTCTGGAGTTGCCAGTCTGATGAGGTTC 320
Db 1392717 CGTTTCATCAATGATGAATAGGATGTTGATCTTTTGGCGCTGAGAGTAAACCGCA 1392658

Qy 321 AAGTCTTGGGCGCTGTTTATACAAATAAGCGCTGTGTGGCGCTGGTATATCTTTTCAAA 380
Db 1392657 AAGTCTTGTACCGTAATGCGGATATCTCCAAAGTAGCGCGCTTACTTCTGGAT 1392598

Qy 381 TTCA 384
Db 1392597 TTCA 1392594

RESULT 6
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match          6.3%; Score 35.2; DB 4; Length 1830121;
Best Local Similarity 49.5%; Pred. No. 4.7;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 201 GCATTTTGTGAGGAGTGCACCGAGGCGCAAGTGCTAAAGCCACCTGCGTTGCTTCT 260
DB 1392777 GAAGTTTATCATGCAAGAACGGCTTCCCTCATCTAATGATCTTGAATATATTTT 1392718

QY 261 CTTTCCATTGAGGAATCTCACAACTATGAGCGCTGGAGTTGCCAGTCTGATGAAGTTCA 320
DB 1392717 CGCTTCATCAATGATGAATAAGGATGGTTTGATCTTTTGGCGCTGAGAGTAAACCGCA 1392658

QY 321 AAGTCCTGGGCTGTTTATACAAATAAGCGCTGTGTTGGCGGTGATATCTTTTGA 380
DB 1392657 AAGTTCTTGTACCGGTAATGCGGATTATCTCCAAAGTAGCGCGGCTTACTTCTGGAT 1392598

QY 381 TTCA 384
DB 1392597 TTCA 1392594

RESULT 7
US-09-165-240-2/c
; Sequence 2, Application US/09165240A
; Patent No. 6087164
; GENERAL INFORMATION:
; APPLICANT: Hochberg, Abraham
; APPLICANT: Ayesh, Suhail
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
; FILE REFERENCE: 9457-0014-999
; CURRENT APPLICATION NUMBER: US/09/165,240A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: US 08/943,608
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-165-240-2

Query Match          6.3%; Score 33.8; DB 3; Length 833;
Best Local Similarity 55.6%; Pred. No. 0.18;
Matches 65; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 78 CCTGAATACCTTCTTCCCTCCATTTATGTGAGAAGGACTCTCCCAAGTGCAATTG 137
DB 775 CCAGAATTCCTGGCCCTGCGCCATTCAGAGCAGGCGCTCCCGAGGCCCCCG 716

QY 138 ACAGGCTCACATGTCCTTTGACATGGAAGCGCACTTTCATTTTCAGTGATCACCA 194
DB 715 CAGGCCCCACCTCCGCGCTGGACAGTTCAGGACACAGTCTCTCTCACCAGCACCA 659

RESULT 8
US-09-568-059-2/c
; Sequence 2, Application US/09568059
; Patent No. 6306833
; GENERAL INFORMATION:
; APPLICANT: Hochberg, Abraham
; APPLICANT: Ayesh, Suhail
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
; FILE REFERENCE: 9457-0014-999
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;
; CURRENT APPLICATION NUMBER: US/09/568,059
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/165,240
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-568-059-2

Query Match          6.3%; Score 33.8; DB 4; Length 833;
Best Local Similarity 55.6%; Pred. No. 0.18;
Matches 65; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 78 CCTGAATACCTTCTTCCCTCCATTTATGTGAGAAGGACTCTCCCAAGTGCAATTG 137
DB 775 CCAGAATTCCTGGCCCTGCGCCATTCAGAGCAGGCGCTCCCGAGGCCCCCG 716

QY 138 ACAGGCTCACATGTCCTTTGACATGGAAGCGCACTTTCATTTTCAGTGATCACCA 194
DB 715 CAGGCCCCACCTCCGCGCTGGACAGTTCAGGACACAGTCTCTCTCACCAGCACCA 659

RESULT 9
US-08-894-324A-1/c
; Sequence 1, Application US/08894324A
; Patent No. 6204437
; GENERAL INFORMATION:
; APPLICANT: Grierson, Donald
; APPLICANT: Blume, Beatrix
; APPLICANT: Hamilton, Andrew
; APPLICANT: Holdsworth, Michael
; APPLICANT: Barry, Cornelius
; TITLE OF INVENTION: DNA Constructs and Plants Incorporating
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca Inc.
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/894,324A
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00564
; FILING DATE: 11-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 95056081.1
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33712
; REFERENCE/DOCKET NUMBER: SEE 45003/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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ORIGINAL SOURCE:
ORGANISM: ACOL PROMOTER
US-08-894-324A-1

Query Match 6.2%; Score 33.4; DB 3; Length 1925;
Best Local Similarity 57.0%; Pred. No. 0.4;
Matches 61; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 419 TCGAGGCTGCTGCTGATGCTGGTGAACCTGCTTACGCTTGTGCTGCTTAACA 478
DB 1856 TGAAGAGATGAATATCAATGTTTGTATGATGATCAAAATATGAGGCTTGAAGGCTATTATA 1797
QY 479 TTGCCACATGATACATCTAAGAAATGTAACCTGTAATAAAAAAAGTTT 525
DB 1796 GTAGAAGATATTAAGTAGAGAAATATAATTAATTAATGAATAATTAATT 1750

RESULT 10

US-09-328-352-2045
Sequence 2045, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2045
LENGTH: 993
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-2045

Query Match 6.2%; Score 33; DB 4; Length 993;
Best Local Similarity 45.5%; Pred. No. 0.38; Indels 0; Gaps 0;
Matches 117; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
QY 230 CAAGTGTAAAGCCACTGGCTTGTCTTCTTCATTCAGGAACCTCAACACTATGAG 289
DB 664 CCAGTTGACAACTATTGTAACCTATTGTTTCTACGAGTCAGAGCTAACCGTTTAATG 723
QY 290 CTTGTGAGTGTGCTGATGAGTCTCAAGTCTCGGCTGCTGCTTGTATACAAATAG 349
DB 724 GAAGCTAAACTTCCACTTCCAGCTTATGAGCAAGCTGTTAAAGCGTCTCATACCTTTAAC 783
QY 350 CGCTGTGCTGGGCTGTATCTTTTGAATTCAGCTTATGAGAGCTGTACTATCT 409
DB 784 TTGCTTGTATGACGTGGCGCAATTTCTGTAAGTGGCTCAACGCTACATTTTACGCTGA 843
QY 410 TGTACCTGCTGCAGGCTGCTGCTGATGCTGGGTGAACACCTGCTTAGGCTTTGCTGTG 469
DB 844 CGTACTTTGGCGGCGCTATGTCACAAAGTTATGTACAGCAGCTGCGAGCTTGGCTTC 903
QY 470 GTAATAACATTTGCCACA 486
DB 904 CCAATGCGACAAACACA 920

RESULT 11

US-08-545-528D-1/c
Sequence 1, Application US/08545528D
Patent No. 6537773
GENERAL INFORMATION:
APPLICANT: Fraser et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB193PI
CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018

PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patent in version 3.1
SEQ ID NO 1
LENGTH: 580073
TYPE: DNA
ORGANISM: Mycoplasma genitalium
US-08-545-528D-1

Query Match 6.0%; Score 32.2; DB 4; Length 580073;
Best Local Similarity 56.0%; Pred. No. 26;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 275 ACTCACAACTATGAGCTGTGGAGTTGCCAGTCTGATGAGGTTCAAAGTCCTGGGCTG 334
DB 476223 ACTTAGAAATTTACACGCTGCTTTGACATCTTATTAAATGTTGAGGCACTGATCATG 476164
QY 335 TTTTATACAAATTAAGCGCTGTGTGGCGGTGATATCTTTTTCGAAATTC 383
DB 476163 AAGGACATATTAAGAGTATTTGTCATTTGATGCTTTTAAATAATAC 476115

RESULT 12

US-09-620-312D-641/c
Sequence 641, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunding
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 641
LENGTH: 2052
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (265) .. (1422)
US-09-620-312D-641

Query Match 5.8%; Score 30.8; DB 4; Length 2052;
Best Local Similarity 51.4%; Pred. No. 3.2;
Matches 71; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 126 CAAGTGCATTTGACAGGCTCACATGCTCTTTGACATGGAACGACCTTCACTTTCACT 185
DB 1923 CAAGCCCACTGCTCCCACTGCTGGAAGGCGCTGCTGCATGCGAGGGCGAGGCTCCCT 1864

RESULT 14
US-08-318-905-19/c
; Sequence 19, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gertin, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/133,803
/ FILING DATE: 06-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 565643land, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27866/32689
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3658
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 569 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 156..304
/
US-08-483-232-19
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Query Match      5.5%; Score 29.6; DB 1; Length 569;
Best Local Similarity 54.6%; Pred. No. 4;
Matches 59; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 100 TCCATTTTATGTGAGAGGACTCTCCCAAGTGCATTTGACAGGCTCACATGTCCTTTGC 159
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
497 TGCCTTTCTATGATATAGAGATGTAAGCAGCAAAATGACTTTCTCAAATTTCTGTTTC 438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 160 ACATGGAAGCGCACTTCACCTTCAGTGCATCCACCAAGCATGCAATTT 207
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
437 AAATGATATACGCTTTGTTCCATTGTAACCACTGGAATAGTTT 390
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Job time : 86 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:49:59 ; Search time 265 Seconds
(without alignments)
6727.279 Million cell updates/sec

Title: US-09-620-607B-34
Perfect score: 535
Sequence: 1 gcagagacacaaatgccaga.....aaaaatgtccctaactgg 535

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2211978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	22.4	742	14	US-10-124-591-2
C 2	94	17.6	445	10	US-09-962-832-63
C 3	94	17.6	445	13	US-09-873-367C-205
4	63.4	11.9	65	13	US-09-908-975-29871
C 5	37.4	7.0	815	13	US-10-027-632-155029
C 6	37.4	7.0	815	14	US-10-027-632-155029
C 7	35.4	6.6	3489	13	US-09-873-367C-444
C 8	35.4	6.6	3497	15	US-10-208-408-36
C 9	35.2	6.6	1830121	15	US-10-329-960-1
10	34.6	6.5	630	13	US-10-027-632-290510
11	34.6	6.5	630	14	US-10-027-632-290510
12	34.2	6.4	630	13	US-10-027-632-290511
13	34.2	6.4	630	14	US-10-027-632-290511
14	33.6	6.3	1204	9	US-09-822-849A-51
15	33.4	6.2	858	13	US-10-027-632-323631

C 16	33.4	6.2	858	14	US-10-027-632-323631
17	33.4	6.2	3681	13	US-10-085-418B-1
18	33	6.2	661	13	US-10-027-632-229516
19	33	6.2	661	13	US-10-027-632-229517
20	33	6.2	661	14	US-10-027-632-229516
21	33	6.2	661	14	US-10-027-632-229517
22	32.6	6.1	6836	15	US-10-076-816-46
23	32.6	6.1	659158	10	US-09-771-208-20
24	32.2	6.0	23580	9	US-09-764-860-990
25	32.2	6.0	23580	13	US-10-212-872-990
26	32.2	6.0	23580	15	US-10-074-095-990
27	32.2	6.0	38459	13	US-09-960-858-3
28	32.2	6.0	38459	13	US-09-960-870-3
C 29	32.2	6.0	580073	13	US-10-205-220-1
30	31.6	5.9	562	9	US-09-864-761-15854
31	31.6	5.9	1125	10	US-09-967-768A-323
32	31.6	5.9	1125	12	US-10-411-010-5
33	31.6	5.9	1125	13	US-09-960-706-1057
34	31.6	5.9	1125	15	US-10-207-655-136
35	31.6	5.9	1340	11	US-09-978-418-43
36	31.6	5.9	2018	10	US-09-822-830A-597
C 37	31.4	5.9	408	11	US-09-918-995-17612
C 38	31.4	5.9	2227	10	US-08-764-877-3516
C 39	31.4	5.9	2227	10	US-09-971-429B-46
C 40	31.4	5.9	2712	13	US-09-764-877-3517
C 41	31.4	5.9	14171	10	US-09-764-877-3518
C 42	31.4	5.9	15998	10	US-09-764-877-3518
43	31	5.8	643	13	US-10-027-632-19603
44	31	5.8	643	14	US-10-027-632-19603
C 45	31	5.8	1621	13	US-10-027-632-258655

ALIGNMENTS

RESULT 1

US-10-124-591-2
; Sequence 2, Appli US/10124591
; Publication No. US20020177208A1
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; Bandman, Olga
; Guegler, Karl J.
; Shah, Purvi
; Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,591
FILING DATE: 16-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/966,317
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0403 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555

Sequence 323631,
Sequence 1, Appli
Sequence 229516,
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Sequence 323, Appli
Sequence 5, Appli
Sequence 1057, Appli
Sequence 136, Appli
Sequence 43, Appli
Sequence 597, Appli
Sequence 17612, A
Sequence 3516, Appli
Sequence 3519, Appli
Sequence 46, Appli
Sequence 3517, Appli
Sequence 3518, Appli
Sequence 19603, A
Sequence 19603, A
Sequence 258655, A

us-09-620-607b-34.rnpb

Mon Dec 22 13:23:38 2003

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Query Match      6.5%; Score 35.2; DB 15; Length 1830121;
Best Local Similarity 49.5%; Pred. No. 43; Indels 0; Gaps 0;
Matches 91; Conservative

QY 201 GCATTTGTCAGGAGTCAACCGAGGCGCAAGTGTAAAGCCACCTGGCTTTCT 260
DB 1392777 GAAGTTATCCATGCAAGAACGCTTGCCTTCATCTAATGATCTTGAATATATTTT 1392718

QY 261 CTTTCCATTCAGGAATCAACAATATAGCCTGTGGAGTTGCCAGTCTGATGAAGGTCA 320
DB 1392717 CGCTTCATCAATGATGAATAAGGATGGTTGATCTTTTGGCGCTGAGAGTAACCGCA 1392658

QY 321 AAGTCCTGGGCTGTTTATACAAATAGCGCTGTGTTGGCGGTGGTATCTTTTCAAA 380
DB 1392657 AAGTCTTGTACCGTAAATGCGGATATCTCCAAAGTAGCGGGCTTACTTCTCGGAT 1392598

QY 381 TTCA 384
DB 1392597 TTCA 1392594

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RESULT 10
US-10-027-632-290510
; Sequence 290510, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290510
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-290510

Query Match      6.5%; Score 34.6; DB 13; Length 630;
Best Local Similarity 58.1%; Pred. No. 0.68; Indels 0; Gaps 0;
Matches 61; Conservative

QY 292 TGTGAGTTGCCAGTCTGATGAAGTTCCTGAGTCTGAGTCTGTTTATACAAATAGCG 351
DB 445 TGTGCTGTGCTCAGATGTAACCTCTGATCTCTGGGCAATTTCTAATAAACATTTT 504

QY 352 CTGCTGTGGCGGTGGTATCTTTTGAATTCAGCTTTTATGAGA 396
DB 505 CTCTGTGATTTTGGTAGGAATCTAAATTCAGCTTTCTCAA 549

RESULT 11
US-10-027-632-290510
; Sequence 290510, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290511
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-290511

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; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290510
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-290510

Query Match      6.5%; Score 34.6; DB 14; Length 630;
Best Local Similarity 58.1%; Pred. No. 0.68; Indels 0; Gaps 0;
Matches 61; Conservative

QY 292 TGTGAGTTGCCAGTCTGATGAAGTTCCTGAGTCTGAGTCTGTTTATACAAATAGCG 351
DB 445 TGTGCTGTGCTCAGATGTAACCTCTGATCTCTGGGCAATTTCTAATAAACATTTT 504

QY 352 CTGCTGTGGCGGTGGTATCTTTTGAATTCAGCTTTTATGAGA 396
DB 505 CTCTGTGATTTTGGTAGGAATCTAAATTCAGCTTTCTCAA 549

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; Sequence 290511, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290511
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-290511

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Db. 479 GACAGAGACTCATCTTAAATGTTCTTGGGTAGAACCAAAAAA 525

Search completed: December 19, 2003, 14:10:51
Job time : 271 secs